

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2003, 09:37:52 ; Search time 38 Seconds
(without alignments)
3513.646 Million cell updates/sec

Title: US-09-637-302C-2

Perfect score: 3413

Sequence: 1 MEHIGQAWKTSINGFGKDA.....AHTEDINACTLTSPRLPVF 648

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3331	97.6	648	11 Q99N57	Q99N57 mus musculus
2	2786.5	81.6	635	13 Q98TC3	Q98TC3 seriola qui
3	2542	74.5	495	11 Q99N58	Q99N58 mus musculus
4	2185	64.0	421	4 Q15278	Q15278 homo sapien
5	2106.5	61.7	420	13 Q90893	Q90893 gallus gall
6	1895.5	55.5	506	15 Q85632	Q85632 avian retro
7	1890.5	55.4	604	11 Q99J44	Q99J44 mus musculus
8	1886	55.3	609	4 Q96115	Q96115 homo sapien
9	1873.5	54.9	375	15 Q67624	Q67624 ic4 retrovi
10	1685	49.4	651	4 Q9Y6T3	Q9Y6T3 homo sapien
11	1675	49.1	359	15 Q85453	Q85453 murine sarc
12	1577	46.2	308	11 Q9CU36	Q9CU36 mus musculus
13	1573	46.1	301	6 Q19055	Q19055 papio hamad
14	1398.5	41.0	307	13 Q90458	Q90458 brachydanio
15	1391.5	40.8	285	13 Q9DEB2	Q9DEB2 seriola qui
16	1384	40.6	739	5 Q9W4Z3	Q9W4Z3 drosophila

ALIGNMENTS

RESULT 1

Q99N57 PRELIMINARY; PRT; 648 AA.
AC Q99N57; Q91WH1;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Protein kinase raf 1 (Similar to murine leukemia viral (V-raf-1)
DE oncogene homolog 1) (3611-MSV).
GN RAF1 OR CRAF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Doi M., Abe S.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Gray T.A., Azama K., Whitmore K.L., Min A., Abe S., Nicholls R.D.;
RT "A conserved gene antisense to the proto-oncogene c-raf encodes a multi-zinc-finger protein, MAKORIN2";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB057663; BAB39743.2; -;
DR EMBL; BC015273; AAH15273.1; -;
DR HSSP; P11345; 1RRR.
DR MGD; MGI:97847; Raf1.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003116; RBD.
DR InterPro; IPR002290; Ser_thr_pkinase.

17 1384 40.6 782 5 Q9NEH9
18 1121.5 32.9 813 5 Q9N4E3
19 982.5 28.8 246 13 Q98TC4
20 853 25.0 177 13 Q90W60
21 801 23.5 180 11 Q99MC6
22 774 22.7 183 13 Q98TC5
23 748 21.9 146 11 Q99N73
24 697 20.4 580 5 Q9GT28
25 604 17.7 283 11 Q9CTT5
26 575 16.8 966 5 Q24170
27 575 16.8 966 5 Q24171
28 569.5 16.7 1003 5 Q24734
29 554 16.2 873 11 Q61097
30 547.5 16.0 373 11 Q9JJU6
31 536 15.7 143 13 Q98TD5
32 525.5 15.4 635 4 Q13476
33 502 14.7 97 11 Q8V185
34 493.5 14.5 553 10 Q81808
35 491.5 14.4 546 10 Q22558
36 488.5 14.3 186 11 Q9DBU7
37 482 14.1 570 10 Q8RWL6
38 466.5 13.7 1030 10 Q9C9U5
39 465 13.6 847 10 Q93XL9
40 459 13.4 771 5 Q19380
41 445.5 13.1 806 10 Q9ZSD8
42 445 13.0 829 10 Q9ZSD9
43 440 12.9 829 10 Q24027
44 433.5 12.7 483 10 Q8RY96
45 429 12.6 903 10 Q9FPR5

Q9neh9 drosophila
Q9n4e3 caenorhabdi
Q98tc4 seriola qui
Q90wg0 seriola qui
Q99mc6 rattus norv
Q98tc5 seriola qui
Q99n73 mus musculu
Q9gt28 brugia mala
Q9ctt5 mus musculu
Q24170 drosophila
Q24171 drosophila
Q24734 drosophila
Q61097 mus musculu
Q9jjju6 mus musculu
Q98td5 seriola qui
Q13476 homo sapien
Q8v185 mus musculu
Q81808 arabidopsis
Q22558 arabidopsis
Q9dbu7 mus musculu
Q8rw16 arabidopsis
Q9c9u5 arabidopsis
Q93xl9 rosa hybrid
Q19380 caenorhabdi
Q9zsd8 lycopersico
Q9zsd9 lycopersico
Q24027 lycopersico
Q8ry96 arabidopsis
Q9fpr5 oryza sativ

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DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00130; DAG_PE_bind; 1.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF02196; RBD; 1.
DR PRINTS: PR00008; DAGPEDOMAIN.
DR ProDom: PD000001; Euk_pkinase; 2.
DR SMART: SM00109; C1; 1.
DR SMART: SM00455; RBD; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase; ATP-binding; Transferase.
SQ SEQUENCE 648 AA; 72917 MW; B70104AEF51C44A5 CRC64;

Query Match      97.6%; Score 3331; DB 11; Length 648;
Best Local Similarity 97.7%; Pred. No. 5.4e-263;
Matches 633; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 MEHIOGAKWTISNGFGKDAVDFGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60
DB 1 MEHIOGAKWTISNGFGLDAVDFGSSCISPTIVQFGYQRRASDDGKLTDSKTSNTIRV 60

QY 61 FLPNKQRTVYVNRNGMSLHDCMLKALKVRLGLOPECCAVFRLHHEHKKARLDWNTDAAS 120
DB 61 FLPNKQRTVYVNRNGMSLHDCMLKALKVRLGLOPECCAVFRLHHEHKKARLDWNTDAAS 120

QY 121 LGEEQLQVDFLDHVPPLTHNFARKTFKLAFCDICQKFLNGFRQCOTGKYFHEHCSKV 180
DB 121 LGEEQLQVDFLDHVPPLTHNFARKTFKLAFCDICQKFLNGFRQCOTGKYFHEHCSKV 180

QY 181 PTMCVDWNSNIQRLFPNNTIGDSGVPALESLTMRMRRESVSRMPVSSQHRYSPPHAF 240
DB 181 PTMCVDWNSNIQRLFPNNTIGDSGVPALESLTMRMRRESVSRMPVSSQHRYSPPHAF 240

QY 241 NTSSPSSEGSLSQORSTSTPNVHMVSTTLVPSDRIEDAIRSHSESASPSSALSSPN 300
DB 241 NTSSPSSEGSLSQORSTSTPNVHMVSTTLVPSDRIEDAIRSHSESASPSSALSSPN 300

QY 301 SPTGWSQKTPVPAQRERAPVSGTQEKNIKIRPRGDRSSYYWEIEASEVMLSTRIGSGSF 360
DB 301 SPTGWSQKTPVPAQRERAPVSGTQEKNIKIRPRGDRSSYYWEIEASEVMLSTRIGSGSF 360

QY 361 GTVYKGKWHGDVAVKILKVVDPTPEQFAFNEVAVLRKTRHVNILLFMGYMTKDNLAIV 420
DB 361 GTVYKGKWHGDVAVKILKVVDPTPEQFAFNEVAVLRKTRHVNILLFMGYMTKDNLAIV 420

QY 421 TQWCEGSSLYKHLHVQETKFOHFQIDIAQTQAGMDYLAHAKNIIRHDMKSNNTFLHEGL 480
DB 421 TQWCEGSSLYKHLHVQETKFOHFQIDIAQTQAGMDYLAHAKNIIRHDMKSNNTFLHEGL 480

QY 481 TVKIGDFGLAVYKSNWSSQVQPTGSLVLMWPEVIRMDNNPFQSDVYSIGVLYE 540
DB 481 TVKIGDFGLAVYKSNWSSQVQPTGSLVLMWPEVIRMDNNPFQSDVYSIGVLYE 540

QY 541 LMTGELPYSHINNRDQIIFVMYGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
DB 541 LMTGELPYSHINNRDQIIFVMYGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600

QY 601 QILSSIELLQSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRPVF 648
DB 601 QILSSIELLQSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRPVF 648

RESULT 2
Q98TC3
ID Q98TC3 PRELIMINARY; PRT; 635 AA.
AC Q98TC3;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
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DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Protein kinase raf 1.
GN CRAF.
OS Seriola quinqueradiata (Five-ray yellowtail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Carangidae; Seriola.
OX NCBI_TaxID=8161;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=GILL;
RA Doi M., Abe S.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=GILL;
RA Gray T.A., Azama K., Whitmore K.L., Min A., Abe S., Nicholls R.D.;
RT "A conserved gene antisense to the proto-oncogene c-Raf encodes a
RT multi-zinc-finger protein, MAKORIN2."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB057654; BAB39747.3; -
DR HSP: P04049; 1FAR.
DR InterPro: IPR002219; DAG_PE_bind.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003116; RBD.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00130; DAG_PE_bind; 1.
DR Pfam: PF00089; pkinase; 1.
DR Pfam: PF02196; RBD; 1.
DR PRINTS: PR00008; DAGPEDOMAIN.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00109; C1; 1.
DR SMART: SM00455; RBD; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; UNKNOWN_1.
DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 635 AA; 71690 MW; A92D0CB8D855DF5B CRC64;

Query Match      81.6%; Score 2786.5; DB 13; Length 635;
Best Local Similarity 82.1%; Pred. No. 1.4e-218;
Matches 532; Conservative 45; Mismatches 58; Indels 13; Gaps 7;

QY 1 MEHIOGAKWTISNGFGKDAVDFGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60
DB 1 MEHIOGAKWTISNGFGKDSAFEG-PCLSPTMVQFGPCQRRSSDDSKMPD-SKTSSTIRV 58

QY 61 FLPNKQRTVYVNRNGMSLHDCMLKALKVRLGLOPECCAVFRLHHEHKKARLDWNTDAAS 120
DB 61 FLPNKQRTVYVNRNGMSLHDCMLKALKVRLGLOPECCAVFRLHHEHKKARLDWNTDAAS 120

QY 59 YLPNQORTVYVNRPGMTLNCLIKALKVRLGLOPECCAVFRLHHEHKKARLDWNTDSTS 118
DB 59 YLPNQORTVYVNRPGMTLNCLIKALKVRLGLOPECCAVFRLHHEHKKARLDWNTDSTS 118

QY 121 LGEEQLQVDFLDHVPPLTHNFARKTFKLAFCDICQKFLNGFRQCOTGKYFHEHCSKV 180
DB 121 LGEEQLQVDFLDHVPPLTHNFARKTFKLAFCDICQKFLNGFRQCOTGKYFHEHCSKV 180

QY 119 LIGQELLVEVLDPVPLTHNFARKTFKLAFCDICQKFLNGFRQCOTGKYFHEHCSKV 178
DB 119 LIGQELLVEVLDPVPLTHNFARKTFKLAFCDICQKFLNGFRQCOTGKYFHEHCSKV 178

QY 181 PTMCVDWNSNIQRLFPNNTIGDSGVPALESLTMRMRRESVSRMPVSSQHRYSPPHAF 240
DB 181 PTMCVDWNSNIQRLFPNNTIGDSGVPALESLTMRMRRESVSRMPVSSQHRYSPPHAF 240

QY 179 PTMCVDWNSNIQRLFPNNTIGDSGVPALESLTMRMRRESVSRMPVSSQHRYSPPHAF 235
DB 179 PTMCVDWNSNIQRLFPNNTIGDSGVPALESLTMRMRRESVSRMPVSSQHRYSPPHAF 235

QY 241 NTSSPSSEGSLSQORSTSTPNVHMVSTTLVPSDRIEDAIRSHSESASPSSALSSPN 300
DB 241 NTSSPSSEGSLSQORSTSTPNVHMVSTTLVPSDRIEDAIRSHSESASPSSALSSPN 300

QY 236 TTPYPTGGGLSQORSTSTPNVHMVSTTLVPSDRIEDAIRSHSESASPSSALSSPN 288
DB 236 TTPYPTGGGLSQORSTSTPNVHMVSTTLVPSDRIEDAIRSHSESASPSSALSSPN 288

QY 301 SPTGWSQKTPVPAQRERAPVSGTQEKNIKIRPRGDRSSYYWEIEASEVMLSTRIGSGSF 360
DB 301 SPTGWSQKTPVPAQRERAPVSGTQEKNIKIRPRGDRSSYYWEIEASEVMLSTRIGSGSF 360

QY 289 SPTGWSQKTPVPAQRERAPVSGTQEKNIKIRPRGDRSSYYWEIEASEVMLSTRIGSGSF 348
DB 289 SPTGWSQKTPVPAQRERAPVSGTQEKNIKIRPRGDRSSYYWEIEASEVMLSTRIGSGSF 348
```

QY 361 GTVYKGWGDVAVKILKVVDPTEQFOAFRNEVAVLRKTRHVNILFMGYMTKONLAI 420
DB 349 GTVYKGWGDVAVKILKVVDPTEQFOAFRNEVAVLRKTRHVNILFMGYMTKONLAI 408
QY 421 TORCEGSSLYKHLHVQETKFOFQOLIDIAQRTAQGMDYLHAKNIHROMKSNFIHEGL 480
DB 409 TORCEGSSLYKHLHVLETFNMQTLQIDIAQRTAQGMDYLHAKNIHROMKSNFIHEGL 468
QY 481 TVKIGDFGLATVKSRWGSQOVQPTGSLVMAPEVIRMOQNNPFSQSDVTSYGLVLYE 540
DB 469 TVKIGDFGLATVKARWGSQOVQPTGSLVMAPEVIRMOQNNPFSQSDVTSYGLVLYE 528
QY 541 LMTGELPYSHNNRQDIIFWVGGRYASPDLSKLYKNCPRKMLVADCVKVKKEERPLFP 600
DB 529 LMTGELPYSHNNRQDIIFWVGGRYASPDLSKLYKNCPRKMLVADCVKVKKEERPLFP 588
QY 601 QILSSITELQHSPLKPNRSASEPLSHRAHTEDINACTLTSPRLPVF 648
DB 589 QILSSITELQHSPLKPNRSASEPLSHRAHTEDINACTLTSPRLPVF 635

RESULT 3

Q99N58 ID Q99N58 PRELIMINARY; PRT; 495 AA.
AC Q99N58
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GN RAF1 OR CRAF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Doi M., Abe S.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RS [2]
RT SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Gray T.A., Azama K., Whitmore K.L., Min A., Abe S., Nicholls R.D.;
RT "A conserved gene antisense to the proto-oncogene c-Raf encodes a
RT multi-zinc-finger protein, MAKORIN2.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB057655; BAB39748.1; -
DR HSSP; P11345; 1RRB.
DR MGD; MGI:97847; Raf1.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003116; RBD.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PF02196; RBD; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00455; RBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase; Serine/threonine-protein kinase.
FT NON_TER 1
FT NON_TER 495

SQ SEQUENCE 495 AA; 55543 MW; B0AB53C2DAA287AE CRC64;
Query Match 74.5%; Score 2542; DB 11; Length 495;
Best Local Similarity 97.8%; Pred. No. 8.3e-199;
Matches 484; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
QY 11 ISNGFGFDKAVDFDSSCISPTIVQOFGYORRASDDGKLTDPSTKSTNTIRVFLPNKQRTVV 70
DB 1 ISNGFGGLKAVDFDSSCISPTIVQOFGYORRASDDGKLTDPSTKSTNTIRVFLPNKQRTVV 60
QY 71 NVNRNGMSLHDCMLKALKVRGLQPECCAVFRLLEHHEGKKARLDWNTDAASLIGELQVDF 130
DB 61 NVNRNGMSLHDCMLKALKVRGLQPECCAVFRLLEHHEGKKARLDWNTDAASLIGELQVDF 120
QY 131 LDHVPPLTHNFAKTEFLKAFCDICQKFLNGFCQTCGKYKFEHCSTKYPTMCDVWSNI 190
DB 121 LDHVPPLTHNFAKTEFLKAFCDICQKFLNGFCQTCGKYKFEHCSTKYPTMCDVWSNI 180
QY 191 RQLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRYSYTPHAFNTSSPSSEGS 250
DB 181 RQLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRYSYTPHAFNTSSPSSEGS 240
QY 251 LSQRQRSTSTPNVHMVSTTLTPVDSRMIEDAIRSHSESASPALSPPNNLSPTGWSQPKT 310
DB 241 LSQRQRSTSTPNVHMVSTTLTPVDSRMIEDAIRSHSESASPALSPPNNLSPTGWSQPKT 300
QY 311 PVPQRERAPVSGTQEKNKIRPRGORDSSYYWEIEASEFVMLSTRIGSGSTGYVYKKGWHG 370
DB 301 PVPQRERAPVSGTQEKNKIRPRGORDSSYYWEIEASEFVMLSTRIGSGSTGYVYKKGWHG 360
QY 371 DVAVKILKVVDPTEQFOAFRNEVAVLRKTRHVNILFMGYMTKONLAIYTCWCESSLY 430
DB 361 DVAVKILKVVDPTEQFOAFRNEVAVLRKTRHVNILFMGYMTKONLAIYTCWCESSLY 420
QY 431 KHLHVQETKFOFQOLIDIAQRTAQGMDYLHAKNIHROMKSNFIHEGLTKVIGDFGLA 490
DB 421 KHLHVQETKFOFQOLIDIAQRTAQGMDYLHAKNIHROMKSNFIHEGLTKVIGDFGLA 480
QY 491 TVKSRWGSQOVQEP 505
DB 481 TVKSRWGSQOVQEP 495

RESULT 4

Q15278 ID Q15278 PRELIMINARY; PRT; 421 AA.
AC Q15278;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
GN RAF1 protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85295973; PubMed=2993863;
RA Bonner T.I., Kerby S.B., Sutcliffe P., Gunnell M.A., Mark G., Rapp U.R.;
RT "Structure and biological activity of human homologs of the raf/mil
RT oncogene.";
RL Mol. Cell. Biol. 5:1400-1407(1985).
CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; L00212; AAA60247.1; JOINED.
DR EMBL; M11376; AAA60247.1; JOINED.
DR EMBL; L00213; AAA60247.1; JOINED.
DR EMBL; L00206; AAA60247.1; JOINED.
DR EMBL; L00207; AAA60247.1; JOINED.
DR EMBL; L00208; AAA60247.1; JOINED.
DR EMBL; L00209; AAA60247.1; JOINED.
DR EMBL; L00210; AAA60247.1; JOINED.
DR EMBL; L00211; AAA60247.1; JOINED.

GN OS Avian retrovirus MH2.
 OC Viruses; Retroviral viruses; Retroviridae; Alpharetrovirus.
 OX NCBI_TaxID=11870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8426123; PubMed=6086317;
 RA Gallibert F., de Dinechin S.D., Righi M., Stehelin D.;
 RT "The second oncogene mil of avian retrovirus MH2 is related to the src
 gene family.";
 RL EMBO J. 3:1333-1338(1984).
 CC -1- SIMILARITY: TO GAG GENE PROTEIN P24 (CORE NUCLEOCAPSID PROTEIN).
 DR EMBL: X00578; CAA25238.1; -;
 DR HSP: P08631; IAD5.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000721; Gag_p24.
 DR InterPro: IPR004040; STV_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00607; Gag_p24; 1.
 DR Pfam: PF00609; pkinase; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00221; STYK; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 KW Core protein; Polyprotein; Tyrosine-protein kinase.
 FT NON_TER 1
 FT CHAIN 127 506
 SQ SEQUENCE 506 AA; 56266 MW; 0583CB415DC06F6C CRC64;
 Query Match 55.5%; Score 1895.5; DB 15; Length 506;
 Best Local Similarity 94.5%; Pred. No. 4.7e-146;
 Matches 361; Conservative 13; Mismatches 7; Indels 1; Gaps 1;
 QY 267 STTLVDSRMIEDAIRSHESASPSALSSPNLSPGTGWSQPKTPVPAQRERAPVSGTQE 326
 DB 126 SPTMPVDSRIELDAIRNSESASPSAGSGSPNNSPGTGWSQPKTPVPAQRERAGTNTQE 185
 QY 327 KNKIPRCQRSSYWEIEASEVLMSTRIGSGFTGYKKGWGDVAVKILKVVDPTEQ 386
 DB 186 KNKIPRCQRSSYWEIEASEVLMSTRIGSGFTGYKKGWGDVAVKILKVVDPTEQ 245
 QY 387 FQAFNEVAVLKRTHVNLFFMGYMTKDNLAIVTQCEGSSLYKHLVQETKFMQLI 446
 DB 246 FQAFNEVAVLKRTHVNLFFMGYMTKDNLAIVTQCEGSSLYKHLVQETKFMQLI 305
 QY 447 DIARTAGMDYLHAKNIIHRDMKSNIFLHEGLTVKIGDFGLATVKSRSWGSGQVQPT 506
 DB 306 DIARTAGMDYLHAKNIIHRDMKSNIFLHEGLTVKIGDFGLATVKSRSWGSGQVQPT 365
 QY 507 GSVLWMAPEVIRMDNPNFQSDVSYGYVLYELMTGELPYSHINNRRDQIIFWVGRYA 566
 DB 366 GSVLWMAPEVIRMDNPNFQSDVSYGYVLYELMTGELPYSHINNRRDQIIFWVGRYA 425
 QY 567 SPDLKLYKNCPKAMKRLVADCKVKEERLPFOILSSIELLOHSLPKINRSASEPSLH 626
 DB 426 SPDLKLYKNCPKAMKRLVADCKVKEERLPFOILSSIELLOHSLPKINRSASEPSLH 485
 QY 627 RAATEDINACTLTSTRLPVF 648
 DB 486 RASHTEDINACTL-TSTRLPVF 506
 RESULT 7
 Q99J44 ID Q99J44 PRELIMINARY; PRT; 604 AA.
 AC Q99J44
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE A-raf.
 GN ARAF.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: BC004757; AA004757.1; -;
 DR HSP: P04049; lFAR.
 DR MGD: MGI:88065; Araf.
 DR InterPro: IPR002219; DAG_pe-bind.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003116; RBD.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00130; DAG_pe-bind; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF02196; RBD; 1.
 DR PRINTS: PR00008; DAGPEDOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00109; C1; 1.
 DR SMART: SM00455; RBD; 1.
 DR SMART: SM00220; S_TK; 1.
 DR SMART: SM00219; TYRK; 1.
 DR PROSITE: PS00479; DAG-pe_bind_DOM_1; 1.
 DR PROSITE: PS00081; DAG-pe_bind_DOM_2; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Serine/threonine-protein kinase; Transferase.
 FT ATP_BIND 1
 SQ SEQUENCE 604 AA; 67581 MW; 05F8262F99DD087 CRC64;
 Query Match 55.4%; Score 1890.5; DB 11; Length 604;
 Best Local Similarity 61.5%; Pred. No. 1.6e-145;
 Matches 376; Conservative 77; Mismatches 125; Indels 33; Gaps 10;
 QY 50 DPSTKSTNTIVLPNKORTVYVNRNGSLHDCLMKALKVRLQPECCAVFRLHEHGKK 109
 DB 13 EPRAVGTVKVLPNKORTVYVNRNGSLHDCLMKALKVRLQPECCAVFRLHEHGKK 69
 QY 110 ARLDWNTDAASLGEELQVDFLDHVPVLTTHNFARKTFLKAFCDICQKFLNGFCQTGC 169
 DB 70 TVTAWDTATAPLDGEBLVEVLEVDVLTWHNFVRKTFESLAFCDICQKFLNGFCQTGC 129
 QY 170 YKFEHCSTKVPVPCVDWS-NITQLLFFNSTIGDSVPALPSLTMRRRESVSRMPVSS 228
 DB 130 YKFEHCSTKVPVPCVDWS-NITQLLFFNSTIGDSVPALPSLTMRRRESVSRMPVSS 178
 QY 229 QHRYSTPHART-----FNTSSPSSEGLSQORORSTSTPNVHMVSTLTPVDSRMIEDAIRS 283
 DB 179 LLTPQGPSPTQORDDEHFSFPANPPLORTNSTPNVHMVSTLTPVDSRMIEDAIRS 238
 QY 284 HSSEA-----SPSALSSPNLSPGTGWSQPKTPVPA-QRERAPVSGTQENKIRPRQ 335
 DB 239 FSTDAAGRGDGAAPRG-SPSPASVS-SGRKSPHSLPSEQRERKSLA--DEKKVKNLGY 294
 QY 336 ROSSYYWEIEASEVLMSTRIGSGFTGYKKGWGDVAVKILKVVDPTEQQAQFNEVA 395
 DB 295 RDSGYTWEVPPSEVQLLKRGTSFGTVPRGMHGDVAVKILKVAQPTAEQAQFNEQ 354
 QY 396 VLKTRHVNILLFMGYMTKDNLAIVTQCEGSSLYKHLVQETKFMQLIDIAQTQAG 455
 DB 355 VLKTRHVNILLFMGYMTKDNLAIVTQCEGSSLYKHLVQETKFMQLIDIAQTQAG 414
 QY 456 MDYLHAKNIIHRDMKSNIFLHEGLTVKIGDFGLATVKSRSWGSGQVQPTGSLWMAPE 515
 DB 415 MDYLHAKNIIHRDMKSNIFLHEGLTVKIGDFGLATVKSRSWGSGQVQPTGSLWMAPE 474
 QY 516 VIRMODNPNFQSDVSYGYVLYELMTGELPYSHINNRRDQIIFWVGRIYASPDLSKLYK 575
 DB 475 VIRMODNPNFQSDVSYGYVLYELMTGELPYSHINNRRDQIIFWVGRIYASPDLSKLYK 534

Db 184 MDYLHAKNIHHRDMKSNINFLHGLTVKIGDFGLATVKSRWGSQVQEQPTGSIILMAPE 243
QY 516 VIRMQDNPFQSDVYSYGVLYELMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYK 575
Db 244 VIRMQDNPFQSDVYSYGVLYELMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYK 303
QY 576 NCPKMKRLVADCKVKKEERPLFPOLISIELLOHSLPKINRSASEPSLHRAHTEDIN 635
Db 304 NCPKMKRLVADCKVKKEERPLFPOLISIELLOHSLPKINRSASEPSLHRAHTEDIN 363
QY 636 ACTLTTSPLRPV 648
Db 364 SCITL-TSTRLPV 375

RESULT 10

QY6T3
ID AC QY6T3 PRELIMINARY; PRT; 651 AA.
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE WUGSC:H_DJ0726N20.3 protein (Fragment).
GN WUGSC:H_DJ0726N20.3
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99063792; PubMed=9847074;
RA Sulston J.E., Waterston R.;
RT "Toward a complete human genome sequence."
RL Genome Res. 8:1097-1108(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Cordes M., Wohldman P., Pape K., Hotic M.;
RT "The sequence of Homo sapiens PAC clone RP4-726N20."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AC006344; RAD43193.1; -;
DR HSSP; P04049; IPR.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003116; RBD.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR004040; STY_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF02196; RBD; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00109; CI; 1.
DR SMART; SM00221; STYK; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Serine/threonine-protein kinase.
FT NON_TER
SQ SEQUENCE 651 AA; 73395 MW; CD2C25EFF7D3E98C CRC64;

Query Match 49.4%; Score 1685; DB 4; Length 651;
Best Local Similarity 54.8%; Pred. No. 1e-128;
Matches 356; Conservative 68; Mismatches 126; Indels 100; Gaps 14;

QY 88 VRGLOPECCAVE-----LLHEHKGKKARLDWNTDAA 119
Db 1 MRGLPECCAVYRQDGPSTINFIHSMRYNIIFCNQERLVSTFFREKPKICWDYDIS 60
QY 120 SLIGELQVDFLDHVPITTHNFARKTFLKAFCDICQKFLNGFRQCOTGKYPKHEGSK 179
Db 61 WLTGELHVEVLENVPLTTHNFVAKTFTFLAFCDFCRKLLFQGFQCOTGKYPKHEGSK 120
QY 180 VPTMCVDSNIRQLLLPNSIGSGVP-----ALPSLTWRMRRESVSRP--VS 227
Db 121 VPLMCVNDYDQD--LLFVSKFEFHHPIQEBASLAETALTSGPSAPASISGPIQITS 178
QY 228 SQHRYSTPHAFTEFTSSPSSSEGLSQRQSTSTNVHMVSTTLVPDSRMIDAIRSHS-- 285
Db 179 PSPSKSIPIQPFPADEHNRQFQDRSSSAPNVH-INTIEPVN---IDDLIRDOGR 234
QY 286 -----ESAPSP-ALSSSPNNL-----SPTGWSO----- 307
Db 235 GDGAPLNQLMRCLRKYSRTSPLLHSVPSEIVDFEPGPVFRGTTGLSATPPASLPGS 294
QY 308 -----PKTPVPAQRERAPVSGTQENKIRPGORDSSYYWEIEASEVMLSTRIGSGSF 360
Db 295 LTNVKAQKSPG-QREKSSSSSEDRNMKTGLRRDSSDDWEIPDQGITVQQRIGSGSF 353
QY 361 GTVYKGWHDVAVYKILKVDPTPEQFAERNEVAVLRKTRHVNILLFMGYMTKDNLAI 420
Db 354 GTVYKGWHDVAVYKILKVDPTPEQFAERNEVAVLRKTRHVNILLFMGYMTKDNLAI 413
QY 421 TQWCEGSSLYKHLHVQETKFOFQIDIAQTACQMDYHLAKNIIHRDMKSNINFLHEGL 480
Db 414 TQWCEGSSLYKHLHVQETKFOFQIDIAQTACQMDYHLAKNIIHRDMKSNINFLHEGL 473
QY 481 TVKIGDFGLATVKSRWGSQVQEQPTGSIILMAPEVIRMODNPNFQSDVYSYGVLYE 540
Db 474 TVKIGDFGLATVKSRWGSQVQEQPTGSIILMAPEVIRMODNPNFQSDVYSYGVLYE 533
QY 541 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPKMKRLVADCKVKKEERPLFP 600
Db 534 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPKMKRLVADCKVKKEERPLFP 593
QY 601 QILSSIELLOHSLPKINRSASEPSLHRAA-HTEDIN--ACTLTTSPLRPV 647
Db 594 QILASSIELLARSPLKINRSASEPSLNRAGFTQEDFSLYAC---ASPKTPI 640
RESULT 11
Q85453
ID Q85453 PRELIMINARY; PRT; 359 AA.
AC Q85453;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 3611 raf gene (Fragment).
OS Murine sarcoma virus.
OC Viruses; Retrovirdae; Retroviridae; Mammalian type C retroviruses.
OX NCBI_TaxID=11802;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84121298; PubMed=6320371;
RA Kan N.C., Flordellis C.S., Mark G.E., Duesberg P.H., Papas T.S.;
RT "A common onc gene sequence transduced by avian carcinoma virus MH2
and by murine sarcoma virus 3611.";
RL Science 223:813-816(1984).
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; K02084; AAA46576.1; -;
DR HSSP; P12931; IFMK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003036; Gag_p30.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR004040; STY_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF02093; Gag_p30; 1.
DR Pfam; PF00069; pkinase; 1.


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DR EMBL: AF006463; AAB63196.1; -.
DR HSP; P12931; IFMK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00221; STYKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR KW Serine/threonine-protein kinase.
FT NON_TER 1
SQ SEQUENCE 301 AA; 34230 MW; 3512983ADP5D1A3B CRC64;

Query Match 46.1%; Score 1573; DB 6; Length 301;
Best Local Similarity 100.0%; Pred. No. 4.4e-120; Mismatches 0; Indels 0; Gaps 0;
Matches 301; Conservative 0;

QY 348 EYMLSTRIGSGFGTVYKKGWGDVAVKILKVVDPTEQFQAFRNEVAVLRKTRHVNIL 407
Db 1 EYMLSTRIGSGFGTVYKKGWGDVAVKILKVVDPTEQFQAFRNEVAVLRKTRHVNIL 60

QY 408 FMGYTKDNLAIYVQCEGSSLYKHLHVQETKFMFQQLIDIAQTAQGM DYLHAKNI IHR 467
Db 61 FMGYTKDNLAIYVQCEGSSLYKHLHVQETKFMFQQLIDIAQTAQGM DYLHAKNI IHR 120

QY 468 DMKSNNIFLHEGLTVKIGDFGLATVKRWSGSGQVEQPTGSLWMAPEVIRMODNPPSF 527
Db 121 DMKSNNIFLHEGLTVKIGDFGLATVKRWSGSGQVEQPTGSLWMAPEVIRMODNPPSF 180

QY 528 QSDVYSYGIVLYELMTGELPYSHINNNDQIIFWVGRGYASPDLSKLYKNCPRAMRLVAD 587
Db 181 QSDVYSYGIVLYELMTGELPYSHINNNDQIIFWVGRGYASPDLSKLYKNCPRAMRLVAD 240

QY 588 CVKVKVEERPLFPQILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRPV 647
Db 241 CVKVKVEERPLFPQILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRPV 300

QY 648 F 648
Db 301 F 301

RESULT 14
Q90458
ID Q90458 PRELIMINARY; PRT; 307 AA.
AC Q90458;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE C-raf protein (Fragment).
GN CRAF OR C-RAF.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRYO;
RA Danilotti J.L.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; X81128; CAA57035.1; -.
DR HSP; P12931; IFMK.
DR ZFIN; ZDB-GENE-990415-41; craf.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
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DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00221; STYKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR KW Tyrosine-protein kinase.
FT NON_TER 1
SQ SEQUENCE 307 AA; 34871 MW; 5B8E3F416F8CB332 CRC64;

Query Match 41.0%; Score 1398.5; DB 13; Length 307;
Best Local Similarity 88.1%; Pred. No. 7.7e-106;
Matches 266; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

QY 347 SEVMLSTRIGSGFGTVYKKGWGDVAVKILKVVDPTEQFQAFRNEVAVLRKTRHVNIL 406
Db 7 NEVLLSRIGSGFGTVHKGWGDVAVKVLKVNPTPEQFQAFRNEVAVLRKTRHVNIL 66

QY 407 LFMGYTKDNLAIYVQCEGSSLYKHLHVQETKFMFQQLIDIAQTAQGM DYLHAKNI IHR 466
Db 67 LFMGYTKDNLAIYVQCEGSSLYKHLHVQETKFMFQQLIDIAQTAQGM DYLMRKHIH 126

QY 467 DMKSNNIFLHEGLTVKIGDFGLATVKRWSGSGQVEQPTGSLWMAPEVIRMODNPPSF 526
Db 127 DMKSNNIFLHEGLTVKIGDFGLATVKRWSGSGQVEQPTGSLWMAPEVIRMODNPPSF 186

QY 527 FQSDVYSYGIVLYELMTGELPYSHINNNDQIIFWVGRGYASPDLSKLYKNCPRAMRLVA 586
Db 187 FQSDVYSYGIVLYELMTGELPYSHINNNDQIIFWVGRGYASPDLSKLYKNCPRAMRLVA 246

QY 587 DCVKVKVEERPLFPQILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRP 646
Db 247 DCVKVKVEERPLFPQILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRP 305

QY 647 VF 648
Db 306 VF 307

RESULT 15
Q9DBE2
ID Q9DBE2 PRELIMINARY; PRT; 285 AA.
AC Q9DBE2;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Protein kinase raf 1 (Fragment).
GN CRAF.
OS Seriola quinqueradiata (Five-ray yellowtail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Carangidae; Seriola.
OX NCBI_TaxID=8161;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=GILL;
RA Doi M., Abe S.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=GILL;
RA Gray T.A., Azama K., Whitmore K.L., Min A., Abe S., Nicholls R.D.;
RT "A conserved gene antisense to the proto-oncogene c-raf encodes a
RT multi-zinc-finger protein, MAKORIN2."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB049965; BAB18860.1; -.
DR HSP; P12931; IFMK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
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DR ProDom: PD000001: Euk_pkinase; 1.
DR SMART: SM00221; STYK; 1.
DR SMART: SM00220; S_TK; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase; Serine/threonine-protein kinase.
FT NON_TER 1
SQ SEQUENCE 285 AA; 32519 MW; 99A692B08A9D4668 CRC64;

Query Match          40.8%; Score 1391.5; DB 13; Length 285;
Best Local Similarity 92.3%; Pred. No. 2.6e-105;
Matches 264; Conservative 11; Mismatches 10; Indels 1; Gaps 1;

QY 363 VYKGKWHGDVAVKILKVVDPTPEQFAFRNEVAVLRKTRHVNILLFMGYMTKONLAIVTQ 422
Db      1 VYKGKWHGDVAVKILKVTDPTPEQFAFRNEVAVLRKTRHVNILLFMGYMTKONLAIVTQ 60

QY 423 WCEGSSLYKHLHVQETKFMQLIDIAQRTAGGMDYLHAKNIHRDMKSNNIFLHEGLTV 482
Db      61 WCEGSSLYKHLHVLETFNFKMIQLIDIAQRTAGGMDYLHAKNIHRDMKSNNIFLHEGLTV 120

QY 483 KIGDFGLATVKSRSWGSOVEQPTGSGVLWMAPEVIRMQDNNPFSQSDVYSYGIVLYELM 542
Db      121 KIGDFGLATVARSWSGSHQVEQPSGSLWMAPEVIRMQDNNPYSFQSDVYSYGIVLYELM 180

QY 543 TGELPYSHINNRDQIIFMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFPQI 602
Db      181 TGELPYSQIANRDQIIFMVGRGYLSPDLSKLYKNCPKAMKRLVADCIKSKDERPLFPQI 240

QY 603 LSSIelloHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRPVF 648
Db      241 LSSIelloHALPKINRSASEPSLHRAAHTEDINACTLT-TSTRLPVF 285
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Search completed: July 9, 2003, 09:46:14
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2003, 09:43:12 ; Search time 22 Seconds
(without alignments)
2831.596 Million cell updates/sec

Title: US-09-637-302C-2
Perfect score: 3413
Sequence: 1 MEHIQAWKTIISNGFGKDA.....AHTEDINACTLTSPRLPVF 648

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.73.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3413	100.0	648	1	TVHUF6
2	3349	98.1	648	1	TVTRRF
3	3249.5	95.2	647	1	S00644
4	2885	84.5	638	1	TVXLRF
5	1927	56.5	602	1	TVTRFR
6	1821.5	55.4	604	1	S00726
7	1889.5	55.4	606	1	TVHUAF
8	1888.5	55.3	380	1	TVFYVM
9	1825	53.5	765	1	TVHUBF
10	1814	53.1	806	1	JN0612
11	1814	53.1	807	1	I51153
12	1654	48.5	333	1	TVMVFF
13	1409.5	41.3	437	1	TVMSRF
14	1398.5	41.0	307	2	S47244
15	1365	40.0	781	1	TVFFDF
16	1338	39.2	1079	1	TVFVMI
17	1336	39.1	450	1	TVFVMR
18	1277	37.4	338	1	TVMSBF
19	1121.5	32.9	813	1	S33261
20	569.5	16.7	1003	2	T13856
21	493.5	14.5	553	2	T04683
22	491.5	14.4	546	2	D84555
23	466.5	13.7	1030	2	F96763
24	455.5	13.3	821	2	T48400
25	440	12.9	829	2	T07406
26	426	12.5	406	2	T52626
27	421	12.3	412	2	T10671
28	421	12.3	963	2	T09911
29	412.5	12.1	568	1	TVFVSI

30	409.5	12.0	736	2	T05137	protein kinase hom
31	407	11.9	528	1	TVFVG9	protein-tyrosine k
32	407	11.9	738	2	F96701	hypothetical prote
33	406	11.9	542	2	A49114	protein-tyrosine k
34	404	11.8	505	2	I38396	protein-tyrosine k
35	404	11.8	541	1	TVCHYS	protein-tyrosine k
36	403	11.8	537	1	A43806	protein-tyrosine k
37	403	11.8	537	1	TVHUSY	protein-tyrosine k
38	403	11.8	1015	2	T00726	probable serine/thr
39	402	11.8	537	2	I51592	protein-tyrosine k
40	401.5	11.8	505	1	S24550	protein-tyrosine k
41	401	11.7	544	2	I51593	protein-tyrosine k
42	400	11.7	982	2	T06576	probable protein k
43	399.5	11.7	509	2	T04688	hypothetical prote
44	398	11.7	475	2	T12955	probable protein k
45	398	11.7	545	2	T05675	hypothetical prote

ALIGNMENTS

RESULT 1
TVHUF6

protein kinase raf-1 (EC 2.7.1.-) - human
N:Alternate names: kinase-related transforming protein raf-1; raf-1 proto-oncogene pr
N:Contains: protein kinase (EC 2.7.1.37)
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 11-Jun-1999
C:Accession: A00637; I57580
R:Bonner, T.I.; Oppermann, H.; Seeburg, P.; Kerby, S.B.; Gunnell, M.A.; Young, A.C.;
Nucleic Acids Res. 14, 1009-1015, 1986
A:Title: The complete coding sequence of the human raf oncogene and the corresponding
A:Reference number: A00637; MUID:86120351; PMID:3003687
A:Accession: A00637
A:Molecule type: mRNA
A:Residues: 1-648 <BON1>
A:Cross-references: GB:X03484; NID:g35841; PIDN:CAA27204.1; PID:g35842
R:Bonner, T.I.; Kerby, S.B.; Suttrave, P.; Gunnell, M.A.; Mark, G.; Rapp, U.R.
Mol. Cell. Biol. 5, 1400-1407, 1985
A:Title: Structure and biological activity of human homologs of the raf/mil oncogene.
A:Reference number: I57580; MUID:85295973; PMID:2993863
A:Accession: I57580
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 228-239, 'L', '241-541', 'I', '543-648 <BON2>
A:Cross-references: GB:L00212; NID:g190837; PIDN:AAA60247.1; PID:g496091
R:Morrison, D.K.; Heidecker, G.; Rapp, U.R.; Copeland, T.D.
J. Biol. Chem. 268, 17309-17316, 1993
A:Title: Identification of the major phosphorylation sites of the Raf-1 kinase.
A:Reference number: A43089; MUID:93352516; PMID:8349614
A:Contents: annotation; phosphorylation sites
A:Note: expression is ubiquitous in mammalian tissues that have been studied
C:Comment: After phosphorylation and activation by protein kinase C and other kinases
C:Genetics:
A:Gene: GDB:RAF1
A:Cross-references: GDB:I19546; OMIM:164760
A:Map position: 3p25-3p25
A:Introns: 278/3; 288/1; 330/3; 370/1; 398/2; 457/2; 473/1; 512/3; 556/3; 601/3
A:Note: the list of introns is incomplete
C:Function:
A:Description: catalyzes the formation of specific peptidyl-threonine-phosphate and p
A:Pathway: MAP kinase cascade
C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; p
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncog
F:139-184/Domain: protein kinase C zinc-binding repeat homology <KIN>
F:347-613/Domain: protein kinase homology <KIN>
F:355-363/Region: protein kinase ATP-binding motif
F:43, 621/Binding site: phosphate (Ser) (covalent) #status experimental
F:139,165,168,184/Binding site: zinc (His, Cys, Cys, Cys, Cys) #status predicted
F:152,155,173,176/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:259/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status experime
F:268/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status exper
F:375/Active site: Lys #status predicted

F:499/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 100.0%; Score 3413; DB 1; Length 648;
Best Local Similarity 100.0%; Pred. No. 2.8e-170;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEHIQAWKTIISNGFGKDAVDFGSSCISPTIVQFGYORRASDGLTDPKTSNTIRV 60
Db 1 MEHIQAWKTIISNGFGKDAVDFGSSCISPTIVQFGYORRASDGLTDPKTSNTIRV 60

Qy 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRLGLOPECCAVFRLLEHKGKARLDWNTDAAS 120
Db 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRLGLOPECCAVFRLLEHKGKARLDWNTDAAS 120

Qy 121 LIGELQVDFLDHVPVLTTHNFARKTFLKLAFCIDICQKFLNGFCOTCGYKPFHCSTKV 180
Db 121 LIGELQVDFLDHVPVLTTHNFARKTFLKLAFCIDICQKFLNGFCOTCGYKPFHCSTKV 180

Qy 181 PTMCVDSNIRQLLPNSTIGDSVGPALPSLTMRRRESVSRMPVSSOHRYSTPHATF 240
Db 181 PTMCVDSNIRQLLPNSTIGDSVGPALPSLTMRRRESVSRMPVSSOHRYSTPHATF 240

Qy 241 NTSSPSEGLSQQRSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSPNNL 300
Db 241 NTSSPSEGLSQQRSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSPNNL 300

Qy 301 SPTGWSQKTPVPAQRERAPVSGTQEKNIIRPGORDSSYYWEIEASEVMLSTRIGSGSF 360
Db 301 SPTGWSQKTPVPAQRERAPVSGTQEKNIIRPGORDSSYYWEIEASEVMLSTRIGSGSF 360

Qy 361 GTVYKKGWGDVAVKILKVVDPTEQFOAFRNEVAVLRTRHVNILLFMGYMTKDLNLAIV 420
Db 361 GTVYKKGWGDVAVKILKVVDPTEQFOAFRNEVAVLRTRHVNILLFMGYMTKDLNLAIV 420

Qy 421 TOWCEGSSLYKHLHVQETKFMQFQIDIAQTQAGMDYLHAKNIIHRDMKSNIFLHEGL 480
Db 421 TOWCEGSSLYKHLHVQETKFMQFQIDIAQTQAGMDYLHAKNIIHRDMKSNIFLHEGL 480

Qy 481 TVKIGDFGLATVKSRWSGQQVEQPTGVLWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
Db 481 TVKIGDFGLATVKSRWSGQQVEQPTGVLWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540

Qy 541 LMTGELPYSHINNRDQIIFWVGRYASPDLSKLYKNCPKAMRLVADCVKVKERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFWVGRYASPDLSKLYKNCPKAMRLVADCVKVKERPLFP 600

Qy 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 2
TVTRFR
protein kinase raf-1 (EC 2.7.1.1) - rat
N:Alternate names: Kinase-related transforming protein raf-1; raf-1 proto-oncogene prote
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 11-Jun-1999
C:Accession: A26126
R:Shikawa, F.; Takaku, F.; Nagao, M.; Sugimura, T.
Mol. Cell. Biol. 7, 1226-1232, 1987
A:Title: Rat c-raf oncogene activation by a rearrangement that produces a fused protein.
A:Reference number: A26126; MUID:87172791; PMID:3550433
A:Accession: A26126
A:Molecule type: mRNA
A:Residues: 1-648 <ISH>
A:Cross-references: GB:M15427; NID:g206544; PIDN:AAA42001.1; PTD:g206545
C:Genetics:
A:Gene: raf
C:Function:
A:Description: signal transduction between cell membrane and nucleus; after phosphorylat
A:Pathway: MAP kinase cascade
A>Note: expression is ubiquitous in mammalian tissues that have been studied
C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; prot

C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncog
F:139-184/Domain: protein kinase C zinc-binding repeat homology <KIN>
F:347-613/Domain: protein kinase homology <KIN>
F:355-363/Region: protein kinase ATP-binding motif
F:43-621/Binding site: phosphate (Ser) (covalent) #status predicted
F:139,165,168,184/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:152,185,173,176/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:259/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predi
F:268/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predi
F:375/Active site: Lys #status predicted
F:499/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predi
F:499/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predi

Query Match 98.1%; Score 3349; DB 1; Length 648;
Best Local Similarity 98.3%; Pred. No. 5.9e-167;
Matches 637; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MEHIOGAWKTIISNGFGKDAVDFGSSCISPTIVQFGYORRASDGLTDPKTSNTIRV 60
Db 1 MEHIOGAWKTIISNGFGKDAVDFGSSCISPTIVQFGYORRASDGLTDPKTSNTIRV 60

Qy 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRLGLOPECCAVFRLLEHKGKARLDWNTDAAS 120
Db 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRLGLOPECCAVFRLLEHKGKARLDWNTDAAS 120

Qy 121 LIGELQVDFLDHVPVLTTHNFARKTFLKLAFCIDICQKFLNGFCOTCGYKPFHCSTKV 180
Db 121 LIGELQVDFLDHVPVLTTHNFARKTFLKLAFCIDICQKFLNGFCOTCGYKPFHCSTKV 180

Qy 181 PTMCVDSNIRQLLPNSTIGDSVGPALPSLTMRRRESVSRMPVSSOHRYSTPHATF 240
Db 181 PTMCVDSNIRQLLPNSTIGDSVGPALPSLTMRRRESVSRMPVSSOHRYSTPHATF 240

Qy 241 NTSSPSEGLSQQRSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSPNNL 300
Db 241 NTSSPSEGLSQQRSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSPNNL 300

Qy 301 SPTGWSQKTPVPAQRERAPVSGTQEKNIIRPGORDSSYYWEIEASEVMLSTRIGSGSF 360
Db 301 SPTGWSQKTPVPAQRERAPVSGTQEKNIIRPGORDSSYYWEIEASEVMLSTRIGSGSF 360

Qy 361 GTVYKKGWGDVAVKILKVVDPTEQFOAFRNEVAVLRTRHVNILLFMGYMTKDLNLAIV 420
Db 361 GTVYKKGWGDVAVKILKVVDPTEQFOAFRNEVAVLRTRHVNILLFMGYMTKDLNLAIV 420

Qy 421 TOWCEGSSLYKHLHVQETKFMQFQIDIAQTQAGMDYLHAKNIIHRDMKSNIFLHEGL 480
Db 421 TOWCEGSSLYKHLHVQETKFMQFQIDIAQTQAGMDYLHAKNIIHRDMKSNIFLHEGL 480

Qy 481 TVKIGDFGLATVKSRWSGQQVEQPTGVLWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
Db 481 TVKIGDFGLATVKSRWSGQQVEQPTGVLWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540

Qy 541 LMTGELPYSHINNRDQIIFWVGRYASPDLSKLYKNCPKAMRLVADCVKVKERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFWVGRYASPDLSKLYKNCPKAMRLVADCVKVKERPLFP 600

Qy 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 3
S00644
protein kinase raf-1 (EC 2.7.1.1) - chicken
N:Alternate names: kinase-related transforming protein raf-1; mht/raf; protein kinase
C:Species: Gallus gallus (chicken)
C:Date: 18-Oct-1989 #sequence_revision 23-Aug-1996 #text_change 11-Jun-1999
C:Accession: S00644; I50380; I50381
R:Koenen, M.; Sippl, A.E.; Trachmann, C.; Blster, K.
Oncogene 2, 179-185, 1988
A:Title: Primary structure of the chicken c-mil protein: identification of domains sh
A:Reference number: S00644; MUID:98217299; PMID:3285296

A:Accession: S00644
A:Molecule type: mRNA
A:Residues: 1-647 <KOE>
A:Cross-references: EMBL:X07017; NID:963232; PIDN:CAA30069.1; PID:g63233
R:Flordellia, C.S.; Kan, N.C.; Lautenberger, J.A.; Samuel, K.P.; Garon, C.F.; Papas, T.S.
Virology 141, 267-274, 1985
A:Title: Analysis of the cellular proto-oncogene mht/raf: Relationship to the 5' sequenc
A:Reference number: 150380; MUID:86098644; PMID:3002017
A:Accession: 150380
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 230-330 <FLO>
A:Cross-references: GB:K03048; NID:g212306; PIDN:AAA48951.1; PID:g212308
R:Jansen, H.W.; Bister, K.
Virology 143, 359-367, 1985
A:Title: Nucleotide sequence analysis of the chicken gene c-mil, the progenitor of the
A:Reference number: 150381; MUID:86045899; PMID:2998016
A:Accession: 150381
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 228-548, 'F', 550-647 <JAN>
A:Cross-references: GB:K03269; NID:g212319; PIDN:AAA48952.1; PID:g212321
C:Genetics:
A:Introns: 278/3; 288/1; 330/3; 370/1; 398/2; 457/2; 473/1; 512/3; 556/3; 601/3
A:Note: the list of introns may be incomplete
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Pathway: MAP kinase cascade
A:Note: after phosphorylation and activation by protein kinase C, phosphorylates and act
C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; prot
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F:139-184/Domain: protein kinase C zinc-binding repeat homology <KIN>
F:347-613/Domain: protein kinase homology <KIN>
F:355-363/Region: protein kinase ATP-binding motif
F:43-621/Binding site: phosphate (Ser) (covalent) #status predicted
F:139,165,168,184/Binding site: zinc (His, Cys, Cys) #status predicted
F:152,155,173,176/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:259/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:268/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted
F:375,393,468,470/Active site: Lys, Glu, Asp, Lys #status predicted
F:499/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 95.28; Score 3249.5; DB 1; Length 647;
Best Local Similarity 94.68; Pred. No. 8.7e-162;
Matches 613; Conservative 20; Mismatches 14; Indels 1; Gaps 1;

Qy 1 MEHQGAWKTSNGFGFKDAVFGDSSCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60
Db 1 MEHQGAWKTSNGFGKDSVDFGPNCSPTIVQOFGYQRRASDDGKISTKSTNTIRV 60

Qy 61 FLPNKQRTVVNVRNGMSLHDLCKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAAS 120
Db 61 FLPNKQRTVVNVRNGMTLHDLCKALKVRGLQPECCAVFRLVTEPKGKVRLDWNTDAAS 120

Qy 121 LIGELQVDFLDHVPFLTHNFARTFLKLAFCDCQKFLNGFCQCGYKFEHCSTKV 180
Db 121 LIGELQVDFLDHVPFLTHNFARTFLKLAFCDCQKFLNGFCQCGYKFEHCSTKV 180

Qy 181 PTMCDVWNIKQLLLFPNSTIGDSVPALPSLTMRKRESVSRMPVSSQHRYSPPHAFTE 240
Db 181 PTMCDVWNIKQLLLFPNSISDSGVPALPLTMRKRESVSRIPVSSQHRYSPPHVFTE 240

Qy 241 NTSPPSSGSLSORQSTSTPNVHMVSTTLFPVDSRMIEDAIRHSESASPSALSSPNNL 300
Db 241 NTSPPSSGTLSORQSTSTPNVHMVSTTMEPDSRIIEDAIRHSESASPSALSSPNNM 300

Qy 301 SPTGNSQKTPVPAQRERAPVSGTOEKNKIRPGORDSSYYWEIEASEVMLSTRIGSGSF 360
Db 301 SPTGNSQKTPVPAQRERAPGNTQENKIRPGORDSSYYWEIEASEVMLSTRIGSGSF 360

Qy 361 GTVYKGKWHGDVAVKILKVDPTPEQFAFRNEAVLKRTHVILLFMGYMTKDLNLAIV 420
Db 361 GTVYKGKWHGDVAVKILKVDPTPEQFAFRNEAVLKRTHVILLFMGYMTKDLNLAIV 420

Qy 421 TQWCESSLYKHLHVQETKQFQMLDIARQTAQGM DYLHAKNIIHRDMKSNFIPLHBEGL 480
Db 421 TQWCESSLYKHLHVQETKQFQMLDIARQTAQGM DYLHAKNIIHRDMKSNFIPLHBEGL 480

Qy 481 TVKIGDFGLATVKSRWSQSQVEQPTGTVLWNAPEVIRMQDNPNPFSFSDVSYGIVLYE 540
Db 481 TVKIGDFGLATVKSRWSQSQVEQPTGTVLWNAPEVIRMQDNPNPFSFSDVSYGIVLYE 540

Qy 541 LMTGELPYSHINNROQIIFWVG RGVSADLSKLYKNCPKAMKRLVADCVKKVKEERPLFP 600
Db 541 LMTGELPYSHINNROQIIFWVG RGVSADLSKLYKNCPKAMKRLVADCLKKVREERPLFP 600

Qy 601 QILSSTIELLQHSPLKINRSASPSLHRAAHTEDINACTLTTPSRPLPVF 648
Db 601 QILSSTIELLQHSPLKINRSASEPSLHRASHTEDINSCITL-TSTRPLPVF 647

RESULT 4
TVXLRP
protein kinase raf-1 (EC 2.7.1.1) - African clawed frog
N:Alternate names: kinase-related transforming protein raf-1; raf-1 proto-oncogene pr
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 11-Jun-1999
C:Accession: S01930; 151254
R:Le Guellec, R.; Le Guellec, K.; Paris, J.; Philippe, M.
Nucleic Acids Res. 16, 10357, 1988
A:Title: Nucleotide sequence of Xenopus C-raf coding region.
A:Reference number: S01930; MUID:89057471; PMID:3194203
A:Accession: S01930
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-638 <LEG>
A:Cross-references: EMBL:X12948; NID:g65027; PIDN:CAA31407.1; PID:g65028
R:Le Guellec, R.; Couturier, A.; Le Guellec, K.; Paris, J.; Le Fur, N.; Philippe, M.
Biol. Cell 72, 39-45, 1991
A:Title: Xenopus c-raf proto-oncogene: cloning and expression during oogenesis and ea
A:Reference number: 151254; MUID:92096753; PMID:1721855
A:Accession: 151254
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-309, 'R', 310-638 <LEX>
A:Cross-references: GB:S74063; NID:g241259; PIDN:AAB20707.1; PID:g241260
C:Genetics:
A:Gene: raf
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threo
A:Pathway: MAP kinase cascade
A:Note: after phosphorylation and activation by protein kinase C, phosphorylates and
C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; p
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncog
F:138-183/Domain: protein kinase C zinc-binding repeat homology <KIN>
F:338-604/Domain: protein kinase homology <KIN>
F:346-354/Region: protein kinase ATP-binding motif
F:43/Binding site: phosphate (Ser) (covalent) #status predicted
F:138,164,167,183/Binding site: zinc (His, Cys, Cys) #status predicted
F:151,154,172,175/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:257/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predi
F:266/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predi
F:366,384,459,461/Active site: Lys, Glu, Asp, Lys #status predicted
F:490/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 84.5%; Score 2885; DB 1; Length 638;
Best Local Similarity 85.3%; Pred. No. 7.5e-143;
Matches 553; Conservative 35; Mismatches 50; Indels 10; Gaps 4;

Qy 1 MEHQGAWKTSNGFGFKDAVFGDSSCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60
Db 1 MEHQGAWKTSNGFGFKESVFEGSSCMSPITVHQFGYQRRASDDGKLTDPKSTNTIRV 60

Qy 61 FLPNKQRTVVNVRNGMSLHDLCKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAAS 120
Db 61 YLPNKQRTVVNVRNGMSLHDLCKMLKVRGLQPECCAVFRLIQDPKG-KLRLDWNTDAAS 119

QY 121 LIGELQVDFLDHVLTHNFARKTKFLKLAFCIDICQKFLNGRCOTCGYKFFHEHCSTKV 180
DB 120 LVGAELQVDFLDHVLTHNFARKTKFLKLAFCIDICQKFLNGRCOTCGYKFFHEHCSTKV 179
QY 181 PTMCVDKSNIRQLLLPNSNIGSGVPALPSLTMRRRESVSRMPVSSQHRVSTPHAFWF 240
DB 180 PTMCVDKSNIRQLLLPNSNIGSGVTPLSLTMRRIGESV-RIPVSSQORVSTPHFPF 238
QY 241 NTSSPSSGLSQRQSTSTPNVHMVSTTLPLVDSRMIEDAIRSHSESASPSALSSPNL 300
DB 239 STSPVSECSLSQRQSTSTPNVHMVSTTMVADSVRIEDALRSHSE-----SGSPNL 291
QY 301 SPFGWSQPKTPVPAQRERAPVSTQKKNKTRPGQRDSSYWEIEASEVMSLSTRIGSGSF 360
DB 292 SPTGWSNAKAPATHREKAASSTGOEKNKTRARGORDSSYWEIIASEVMSLSTRIGSGSF 351
QY 361 GTVYKKGWHDGVAVKILKVVDPTPEQFOAFRNEVAVLRTRHVNILFLFGYMTKDLAI 420
DB 352 GTVYKKGWHDGVAVKILKVTDPTPEQLOAFRNEVAVLRTRHVNILFLFGYMTKDLAI 411
QY 421 TOMCEGSSLYKHLHVQETKFMQFOLIDIAQTAGQMDYLHAKNI IHRDMKSNIFLHEGL 480
DB 412 TOMCEGSSLYKHLHVLTDFOMFOLIDIAQTAGQMDYLHAKNI IHRDMKSNIFLHEGL 471
QY 481 TVKIGDEGLATVKSRSWGSQOQPTGSLVWMAPEVIRMQDNNPFQSDVTSYGIVLYE 540
DB 472 TVKIGDEGLATVKSRSWGSQOQPTGSLVWMAPEVIRMQDNNPFQSDVTSYGIVLYE 531
QY 541 LMTGELPYSHINNRDQIIFMVGGRYASPDLSKLYKNCPRKMLVADCKVKEERPLPP 600
DB 532 LMTGELPYSHINNRDQIIFLVGGRVVPDLSKLYKNCPRKMLVADCKVKEERPLPP 591
QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTITTS 648
DB 592 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDISSCAL-TSTRLPVF 638

RESULT 5
TVTRRR
protein kinase (EC 2.7.1.37) raf - rat
N:Alternate names: Kinase-related transforming protein raf; raf proto-oncogene protein-s
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 11-Jun-1999
C:Accession: B26126
R:Ishikawa, F.; Takaku, F.; Nagao, M.; Sugimura, T.
Mol. Cell. Biol. 7, 1226-1232, 1987
A:Title: Rat c-raf oncogene activation by a rearrangement that produces a fused protein.
A:Reference number: A26126; MUID:87172791; PMID:3550433
A:Accession: B26126
A:Molecule type: mRNA
A:Cross-references: GB:M15428; NID:G206546; PIDN:AAA42002.1; PID:G206547
C:Genetics:
C:Superfamily: rat protein kinase raf; protein kinase homology
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonine
F:301-567/Domain: protein kinase homology <kin>
F:309-317/Region: protein kinase ATP-binding motif
F:329/Active site: Lys #status predicted
F:453/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 56.5%; Score 1927; DB 1; Length 602;
Best Local Similarity 79.4%; Pred. No. 4.3e-93;
Matches 386; Conservative 22; Mismatches 54; Indels 24; Gaps 4;

QY 173 HECSTKVPKTMCDVMSNIRQLLLFPNSTIGD-----SGVPALPSLTMRRRESVS 222
DB 131 NERLSEQVEYLEDYKRLNEKLESNTKGEQLKLDELQASDV-----TVYRERKLQE 186
QY 223 RMPVSSQHRVSTPHAFPTNTSSPSSGLSQRQSTSTPNVHMVSTTLPLVDSRMIEDAIR 282
DB 187 KELLHNONSW-----LNTLTKTKTDELLALGREGKNEILELKTCT---LENKKEADAIR 236

QY 283 SHSESASPSALSSSPNNLSPTGWSQPKTPVPAQRERAPVSTQKKNKTRPGQRDSSYWM 342
DB 237 SHSESASPSALSSSPNNLSPTGWSQPKTPVPAQRERAPVSTQKKNKTRPGQRDSSYWM 296
QY 343 ETEASEVMSLSTRIGSGSFVYKKGWHDGVAVKILKVVDPTPEQFOAFRNEVAVLRTRH 402
DB 297 ETEASEVMSLSTRIGSGSFVYKKGWHDGVAVKILKVVDPTPEQLOAFRNEVAVLRTRH 356
QY 403 VNILFMGYMTKDLAIYVTOCEGSSLYKHLHVQETKFMQFOLIDIAQTAGQMDYLHAK 462
DB 357 VNILFMGYMTKDLAIYVTOCEGSSLYKHLHVQETKFMQFOLIDIAQTAGQMDYLHAK 416
QY 463 NIIHRDMKSNIFLHEGLTVKIGDEGLATVKSRSWGSQOQPTGSLVWMAPEVIRMQDN 522
DB 417 NIIHRDMKSNIFLHEGLTVKIGDEGLATVKSRSWGSQOQPTGSLVWMAPEVIRMQDN 476
QY 523 NPFQSDVTSYGIVLYEELMTGELPYSHINNRDQIIFMVGGRYASPDLSKLYKNCPRKAM 582
DB 477 NPFQSDVTSYGIVLYEELMTGELPYSHINNRDQIIFMVGGRYASPDLSKLYKNCPRKAM 536
QY 583 RLVAQCVKVKKEERPLFPQILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTITTS 642
DB 537 RLVAQCVKVKKEERPLFPQILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTITTS 596
QY 643 PRLPVF 648
DB 597 PRLPVF 602

RESULT 6
S00726
protein kinase A-raf-1 (EC 2.7.1.1) - rat
N:Alternate names: A-raf-1 proto-oncogene protein-serine/threonine kinase; kinase-rel
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence_revision 23-Aug-1996 #text_change 11-Jun-1999
C:Accession: S00726
R:Ishikawa, F.; Takaku, F.; Nagao, M.; Sugimura, T.
Oncogene Res. 1, 243-253, 1987
A:Title: The complete primary structure of the rat A-raf cDNA coding region: conserva
A:Reference number: S00726; MUID:88217324; PMID:3449797
A:Accession: S00726
A:Molecule type: mRNA
A:Residues: 1-604 <ISH>
A:Cross-references: EMBL:X06942; NID:G55756; PIDN:CAA30023.1; PID:G55757
C:Function:
A:Description: signal transduction between cell membrane and nucleus; after phosphory
A:Pathway: MAP kinase cascade
A:Note: in mouse, expressed in urogenital tissues and, at lower levels, in other tiss
C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; p
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncog
F:99-144/Domain: protein kinase C zinc-binding repeat homology <kin>
F:306-572/Domain: protein kinase homology <kin>
F:314-322/Region: protein kinase ATP-binding motif
F:99-125,128,144/Binding site: zinc (His, Cys, Cys) #status predicted
F:112,115,133,136/Binding site: zinc (Cys, His, Cys) #status predicted
F:214/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:223/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predi
F:334/Active site: Lys #status predicted
F:580/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 55.4%; Score 1891.5; DB 1; Length 604;
Best Local Similarity 61.7%; Pred. No. 3e-91;
Matches 377; Conservative 76; Mismatches 125; Indels 33; Gaps 10;

QY 50 DPSTSTNIRVFLPNKORTVVNVRGMSLHDLCKALKVRLQPECCAVFRLHEHGKK 109
DB 13 EPSSAVGTAVKYLPNKORTVVNVRGMSVDSLDKALKVRLQDCCVYRLI---KGR 69
QY 110 ARLDNNTDAASLIGEEQLQVDFLDHVLTHNFARKTKFLKLAFCIDICQKFLNGRCOTCG 169
DB 70 TVTAMDTAIPLDGEELIVELEDVPLTMHNFVRKTFSSLAFCDFCLKFLFHCRCOTCG 129

QY 170 YKFEHCSTKVTPTMCVDWS-NIRQLLPNPSTIGSGVPALPSLTMRRRESVSRMPVSS 228
Db 130 YKFEHCSSKVTPTVCVDMSTNRQFYHSIQDLGSGS-----RQEVPSNLVSYNE 178
QY 229 QHRYSTPHAFV-----FNTSSPSSSEGLSORSTSTPNVHMVSTTLPTVDSRMIEDAIRS 283
Db 179 LLTPQCPSPFTQQRDOEHFSPAPNPPLQIRISTSTPNVHMVSTTAPMDSSLMQFTQAQ 238
QY 284 HSESA-----SPSALSSSPNNLSPTGWSQPKTPVPA-QRERAPVSGTOEKKIRPRGQ 335
Db 239 FSTDAAGRGDGPAG-SPSPASVS-SGRKSPHSKLPAEQREKSLA--DEKKVKNLGY 294
QY 336 RDSYVYIEASEVMSLSTRIGSGFGVYKKGWGDVAVKILKVVDPPTPQFQAFRNEVA 395
Db 295 RDSGYVYVPEVSEVQLKRIGTSGFTVFRGHWGDVAVKVLVKAQPTAEQAQAFKNEQ 354
QY 396 VLKTRHVNILLFMGYMTKDLAIWTCWCESSLYKHLVQETKQFQFOLIDIAAROTAQ 455
Db 355 VLKTRHVNILLFMGYMTKQFALITQWCESSLYHHLVADTRFDVQLIDVARQTAQ 414
QY 456 MDYLHAKNIIHRDKMNSNIFLHEGLTVKIGDFGLATVKSWSGSGQVQPTGSLYMAPE 515
Db 415 MDYLHAKNIIHRDKMNSNIFLHEGLTVKIGDFGLATVKTWSGAQPLEQPSGSLYMAAE 474
QY 516 VIRMDNPFQSDVTSYGIVLYELMTGELPYSHINNROQIFMVGRGYASPDLSKLYK 575
Db 475 VIRMDNPFQSDVTAIGVLYELMTGSLPYSHIGSDQOIFMVGRGYASPDLSKIFS 534
QY 576 NCPKAMRLVADCVKVKKEERPLFPQILSLTELQHSPLKPNRSASEPSLHRAHTEIDIN 635
Db 535 NCPKAMRLVADCVKVKKEERPLFPQILSLTELQHSPLKPNRSASEPSLHRAHTEIDIN 635
QY 636 ACTLTSPLRP 646
Db 594 ACLLSAARLVP 604

RESULT 7

TVHDAF
N: protein kinase A-raf-1 (EC 2.7.1.1) - human
A: Alternate names: A-raf-1 proto-oncogene protein-serine/threonine kinase; kinase-related
C: Species: Homo sapiens (man)
C: Date: 31-Dec-1988 #sequence-revision 14-Jul-1994 #text_change 16-Jun-2000
A: Accession: A53026; A26439; A23541
R: Lee, J.E.; Beck, T.W.; Brennscheidt, U.; DeGennaro, L.J.; Rapp, U.R.
Genomics 20, 43-55, 1994
A: Title: The complete sequence and promoter activity of the human A-raf-1 gene (ARAF1).
A: Reference number: A53026; MUID: 94292185; PMID: 8020955
A: Accession: A53026
A: Status: not compared with conceptual translation
A: Molecule type: DNA
A: Residues: 1-606 <LEE>
A: Cross-references: GB:L24038; NID:g508473; PIDN:AAA65219.1; PID:g780127
R: Beck, T.W.; Huleihel, M.; Gannell, M.; Bonner, T.I.; Rapp, U.R.
Nucleic Acids Res. 15, 595-609, 1987
A: Title: The complete coding sequence of the human A-raf-1 oncogene and transforming act
A: Reference number: A26439; MUID: 87146380; PMID: 3029685
A: Accession: A26439
A: Molecule type: mRNA
A: Residues: 1-297, 'x', 299-606 <BEC>
A: Cross-references: EMBL:X04790; NID:g28820; PIDN:CAA28476.1; PID:g1340152
R: Mark, G.E.; Sealey, T.W.; Shows, T.B.; Mountz, J.D.
Proc. Natl. Acad. Sci. U.S.A. 83, 6312-6316, 1986
A: Title: pks, a raf-related sequence in humans.
A: Reference number: A23541; MUID: 86313571; PMID: 3529082
A: Accession: A23541
A: Molecule type: mRNA
A: Residues: 292-367, 'p', 369-377, 'v', 379-468, 'p', 470-477, 't', 479-589 <MAR>
A: Cross-references: GB:M13829; NID:g189999; PIDN:AAB08754.1; PID:g387023
C: Genetics:
A: Gene: GDB:ARAF1
A: Cross-references: GDB:l19004; OMIM:311010
A: Map position: Xp11.3-Xp11.23

A: Introns: 32/3; 67/2; 101/3; 153/2; 186/2; 230/3; 240/1; 288/3; 356/2; 415/2; 431/1;
C: Function:
A: Description: signal transduction between cell membrane and nucleus; after phosphory
A: Pathway: MAP kinase cascade
A: Note: in mouse, expressed in urogenital tissues and, at lower levels, in other tiss
C: Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; p
C: Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncog
F: 99-144/Domain: protein kinase C zinc-binding repeat homology <K2N>
F: 308-574/Domain: protein kinase homology <KIN>
F: 316-324/Region: protein kinase ATP-binding motif
F: 99,125,128,144/Binding site: zinc (His, Cys, Cys) #status predicted
F: 112,115,133,136/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F: 214/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F: 223/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predi
F: 336/Active site: Lys #status predicted
F: 582/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 55.4%; Score 1889.5; DB 1; Length 606;
Best local Similarity 61.9%; Pred. No. 3.8e-91;

Matches 376; Conservative 76; Mismatches 132; Indels 23; Gaps 9;

QY 50 DPSTSTNTIRVLPNKORTVNVNRGMSLHDCMLKALKVGRLOPECCAVFRLHEHKGK 109
Db 13 EPSRAVTVKYLVPNKQRTVVVRDMSVIDSLDKALKVGRLOPECCAVFRLHEHKGK 69
QY 110 ARLDWNTDAASLIGEELQVDFLDHVPVLTTHNFARKTFLKAFCDICQKELLNGFRQTCG 169
Db 70 TVTAWDTATADLGEELIVELEVDVPLTMHNFVKRTFFSLAFCDCLFELHGFRCQTCG 129
QY 170 YKFEHCSTKVTPTMCVDWSNIRQLLPNPSTIGSGVPALPSLTMRRRESVSRMPVSS 228
Db 130 YKFEHCSSKVTPTVCVDMSTNRQFYHSIQDLGSGS-----RQEVPSNLVSYNE 187
QY 229 QHRYSTPHAFV-----FNTSSPSSSEGLSORSTSTPNVHMVSTTLPTVDSRMIEDAIRS 283
Db 179 LLTPQCPSPFTQQRDOEHFSPAPNPPLQIRISTSTPNVHMVSTTAPMDSSLMQFTQAQ 238
QY 284 HSESA-----SPSALSSSPNNLSPTGWSQPKTPVPA-QRERAPVSGTOEKKIRPRGQ 335
Db 239 FSTDAAGRGDGPAG-SPSPASVS-SGRKSPHSKLPAEQREKSLA--DEKKVKNLGY 294
QY 336 RDSYVYIEASEVMSLSTRIGSGFGVYKKGWGDVAVKILKVVDPPTPQFQAFRNEVA 395
Db 295 RDSGYVYVPEVSEVQLKRIGTSGFTVFRGHWGDVAVKVLVKAQPTAEQAQAFKNEQ 354
QY 396 VLKTRHVNILLFMGYMTKDLAIWTCWCESSLYKHLVQETKQFQFOLIDIAAROTAQ 455
Db 355 VLKTRHVNILLFMGYMTKQFALITQWCESSLYHHLVADTRFDVQLIDVARQTAQ 414
QY 456 MDYLHAKNIIHRDKMNSNIFLHEGLTVKIGDFGLATVKSWSGSGQVQPTGSLYMAPE 515
Db 415 MDYLHAKNIIHRDKMNSNIFLHEGLTVKIGDFGLATVKTWSGAQPLEQPSGSLYMAAE 474
QY 516 VIRMDNPFQSDVTSYGIVLYELMTGELPYSHINNROQIFMVGRGYASPDLSKLYK 575
Db 475 VIRMDNPFQSDVTAIGVLYELMTGSLPYSHIGSDQOIFMVGRGYASPDLSKIFS 534
QY 576 NCPKAMRLVADCVKVKKEERPLFPQILSLTELQHSPLKPNRSASEPSLHRAHTEIDIN 635
Db 535 NCPKAMRLVADCVKVKKEERPLFPQILSLTELQHSPLKPNRSASEPSLHRAHTEIDIN 635
QY 636 ACTLTSPLRP 646
Db 594 ACLLSAARLVP 604

RESULT 8

TVFVMM
N: protein kinase (EC 2.7.1.37) m1l - avian myelocytomatosis virus MH2
A: Alternate names: kinase-related transforming protein m1l (mht); m1l proto-oncogene
C: Species: avian myelocytomatosis virus MH2
A: Note: host Gallus gallus (chicken)
C: Date: 27-Nov-1985 #sequence-revision 27-Nov-1985 #text_change 23-Feb-1997

Db 100 ESLNGTDFSVSSASMDVTYSSSSSLVLPSSLSVFQNTDVARSNPKSPQKPIVRVF 159
QY 62 LPNKQRTVVNVNRMGSLHDCIMKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAASL 121
Db 160 LPNKQRTVVNRCVTVRDSLKALMMGLIPECCAVYRI--QDGEKKPIGWDIDISWL 216
QY 122 IGEELQVDFLDHVPITTHNFARKTFLKAFCDICQKFLNGFCQTCGYKHEHCSTKVP 181
Db 217 TGEELHVEVLENVLTTHNFVRKTFFTLAFCDFCRKLQFGFCQTCGYKHEHCSTKVP 276
QY 182 TMCVDWSNIRQLLPNPTGDSVP-----ALPDLMMRMRESVRMP--VSSQ 229
Db 277 LMCVNYDQLD--LLFVSFFEHPIPOEASLAETALTSGPSAPASDSIGPQILSPS 334
QY 230 HRYSTPHAFNTWSSPSSEGLSQQRSTSTPNVMVSTTLVPDSRMIEDAIRS--HSE 286
Db 335 PSKSIPIQPPFPADEDRHNOFGQRDRSSAPNVH-INTIEPVN---IDDLIRQDQGRGD 390
QY 287 SASPSALSSSPNNLSPGMSQ----PKTPVPAQERAPVSTQEKNIIRPGQRDSYYW 342
Db 391 GGTGLSATPPASLPGLSTNVKALQKSPGP-QREKSSSSSEDRNRKMTLGRDRSDDW 449
QY 343 EIEASEMLSTRIGSGSGTGYKQKWHGDVAVKILKVDPTPEQFQAFRNEVAVLRKTRH 402
Db 450 EIPDQGITVGRIGSGSGTGYKQKWHGDVAVKMLNVTAPTQQLQAFKNEVGLRTRH 509
QY 403 VNILLFMGYMKNLAIVTQCEGSSLYKHLHVQETKQFQMLDIAAQAGMDYLHAK 462
Db 510 VNILLFMGYSTKPKQLAIVTQCEGSSLYKHLHVQETKQFQMLDIAAQAGMDYLHAK 569
QY 463 NIIHRDKSNIFLHEGLTVKIGDFGLATVKRSWGSQVQEQPTGSLVMAPEVIRMQDN 522
Db 570 SLIHRDKSNIFLHEGLTVKIGDFGLATVKRSWGSQVQEQPTGSLVMAPEVIRMQDN 629
QY 523 NPFSQSDVYIGVLYELMTGELPYSHINNRDQIIFMVGSGYASPDLSKLYKNCPRAMK 582
Db 630 NPFSQSDVYAFGIYVLYELMTGQLPYSHINNRDQIIFMVGSGYASPDLSKLYKNCPRAMK 689
QY 583 RLAVDCVKKVEERPLFPQILSSLELQHSPLKINRASEPSLHRAA-HTEDIN--ACTL 639
Db 690 RLMAECLKKRDERPLFPQILASIELLARSUPKIHRSASEPSLNRAGFQTEDFSLEYAC-- 747
QY 640 TTSPLPV 647
Db 748 -ASPKTPI 754

RESULT 10
JN0612
protein kinase B-raf (EC 2.7.1.-), long form - chicken
N;Alternate names: kinase-related transforming protein B-raf; protein kinase Rml1; trans
N;Contains: protein kinase B-raf, short form
C;Species: Gallus gallus (chicken)
C;Date: 24-Feb-1994 #sequence_revision '23-Aug-1996 #text_change 11-Jun-1999
C;Accession: JN0612; S31792
R;Calogeraki, I.; Barnier, J.V.; Eyche, A.; Felder, M.P.; Calothy, G.; Marx, M.
Biochem. Biophys. Res. Commun. 193, 1324-1331, 1993
A;Title: Genomic organization and nucleotide sequence of the coding region of the chicken
A;Reference number: JN0612; MUID:93312327; PMID:832353
A;Accession: JN0612
A;Molecule type: DNA
A;Residues: 1-806 <CAL>
A;Cross-references: EMBL:X67052; NID:963339; PIDN:CAA47436.1; PID:963340
C;Genetics:
A;Gene: c-Rml1
A;Introns: 46/3; 80/3; 168/3; 203/2; 237/3; 287/2; 327/2; 380/2; 393/1; 433/1; 478/3; 51
C;Function:
A;Description: member of signal transduction pathway(s) activated by nerve growth factor
A;Pathway: MAP kinase cascade
C;Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; prot
C;Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotrans
nc
F;1-806/Product: protein kinase B-raf, long form #status predicted <MAT>

F;1-392,433-806/Product: protein kinase B-raf, short form #status predicted <SHE>
F;235-280/Domain: protein kinase C zinc-binding repeat homology <XZ>
F;495-761/Domain: protein kinase homology <XIN>
F;503-511/Region: protein kinase ATP-binding motif
F;235,261,264,280/Binding site: zinc (His, Cys, Cys) #status predicted
F;248,251,269,272/Binding site: zinc (His, Cys, His, Cys) #status predicted
F;365,647/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predi
F;373/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predi
F;523/Active site: Lys #status predicted
F;769/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 53.1% Score 1814; DB 1; Length 806;
Best Local Similarity 52.8% Pred. No. 4.4e-87;
Matches 382; Conservative 80; Mismatches 149; Indels 112; Gaps 15;
QY 9 KTSNGFGFK-----DAVFDGSSCISPIVQFGYORASDDGLTDPKSTNIRVF 61
Db 101 ESMGNGTDFSVSSASDTVTASSSSSLSVAPSSSLSYQNTDNRNPKSPQKPIVRVF 160
QY 62 LPNKQRTVVNVNRMGSLHDCIMKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAASL 121
Db 161 LPNKQRTVVNRCVTVRDSLKALMMGLIPECCAVYRI--QDGEKKPIGWDIDISWL 217
QY 122 IGEELQVDFLDHVPITTHNFARKTFLKAFCDICQKFLNGFCQTCGYKHEHCSTKVP 181
Db 218 TGEELHVEVLENVLTTHNFVRKTFFTLAFCDFCRKLQFGFCQTCGYKHEHCSTKVP 277
QY 182 TMCVDWSNIRQLLPNPTGDSVP-----ALPDLMMRMRESVRMP--VSSQ 229
Db 278 LMCVNYDQLD--LLFVSFFEHPIPOEASLAETALTSGPSAPASDSIGPQILSPS 333
QY 216 RMRESVRMPVSSQHYSTPHAFNTWSSPSSEGLSQQRSTSTPNVMVSTTLVPDSR 275
Db 334 -----PSPSK---SIPIQPPFPADEDRHNOFGQRDRSSAPNVH-INTIEPVN-- 378
QY 276 MIEDAIRSHS-----ESASPSAL- 293
Db 379 -IDDLIRQDQGRGEGAPLNQLMRLKRYQSRTPSLLHSPSEIVDFEPGVPFRCSTAG 437
QY 294 -----SSSPNNLSPGMSQVTPVPAQERAPVSTQEKNIIRPGQRDSYYWEIAS 347
Db 438 LSATPPASLPGLSTNVKALQ-KSPGP-QREKSSSSSEDRNRKMTLGRDRSDDW 495
QY 348 EVMSTRIGSGSGTGYKQKWHGDVAVKILKVDPTPEQFQAFRNEVAVLRKTRHYNILL 407
Db 496 QITVGRIQSGSGTGYKQKWHGDVAVKMLNVTAPTQQLQAFKNEVGLRTRHYNILL 555
QY 408 FMGYMKNLAIVTQCEGSSLYKHLHVQETKQFQMLDIAAQAGMDYLHAKNIIHR 467
Db 556 FMGYSTKPKQLAIVTQCEGSSLYKHLHVQETKQFQMLDIAAQAGMDYLHAKNIIHR 615
QY 468 DMKSNIFLHEGLTVKIGDFGLATVKRSWGSQVQEQPTGSLVMAPEVIRMQDNPPFS 527
Db 616 DLKSNIFLHEGLTVKIGDFGLATVKRSWGSQVQEQPTGSLVMAPEVIRMQDNPPFS 675
QY 528 QSDVYIGVLYELMTGELPYSHINNRDQIIFMVGSGYASPDLSKLYKNCPRAMKRLVAD 587
Db 676 QSDVYAFGIYVLYELMTGQLPYSHINNRDQIIFMVGSGYASPDLSKLYKNCPRAMKRLMAE 735
QY 588 CVKKVKEERPLFPQILSSLELQHSPLKINRASEPSLHRAA-HTEDIN--ACTLTSR 644
Db 736 CLAKKDERPLFPQILASIELLARSUPKIHRSASEPSLNRAGFQTEDFSLEYAC---ASPK 792
QY 645 LPV 647
Db 793 TPI 795

RESULT 11

I51153
protein kinase B-raf (EC 2.7.1.-), long splice form - quail
N;Alternate names: kinase-related transforming protein B-raf; protein kinase Rml1; tr
N;Contains: protein kinase B-raf, short splice form

C:Species: Coturnix coturnix (quail)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 11-Jun-1999
C:Accession: I51153; I51152
R:Eychene, A.; Barnier, J.
Oncogene 7, 1315-1323, 1992
A:Title: Quail neuroretina c-Rn11(B-raf) protooncogene cDNAs encode two proteins of 93.5
A:Reference number: I51152; MUID:92319540; PMID:1620546
A:Accession: I51153
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-807 <EVC>
A:Cross-references: GB:M80846; NID:g213600; PIDN:AAA49493.1; PID:g213601
A:Accession: I51152
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-392,433-807 <EY2>
A:Cross-references: GB:M80845; NID:g213598; PIDN:AAA49492.1; PID:g213599
C:Genetics:
A:Gene: c-Rn11
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Pathway: MAP kinase cascade
A:Note: believed to phosphorylate MAP kinase kinase; found in hippocampal neurons and de
C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homologs; prot
C:Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotrans
nc
F:1-392,433-807/Product: protein kinase B-raf, short splice form #status predicted <MAY2
F:235-280/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F:495-761/Domain: protein kinase C homology <KIN>
F:503-511/Region: protein kinase ATP-binding motif
F:235,261,264,280/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:248,251,269,272/Binding site: zinc (Cys, Cys, His, His) #status predicted
F:365,647/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predict
F:373/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predict
F:523,541,616,618/Active site: Lys, Glu, Asp, Lys #status predicted
F:769/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 53.1%; Score 1814; DB 1; Length 807;
Best Local Similarity 52.8%; Pred. No. 4.5e-87;
Matches 382; Conservative 80; Mismatches 149; Indels 112; Gaps 15;

Qy 9 KTSINGGFK-----DAVFGDGGISPTIVQQFGQRRASDDGKLTDPKTSNIRVF 61
Db 101 ESMGNGTDFSVSSASTDTVASSSSLSVAPSSLSVYQNPDMRNPKSQKPIRVF 160
Qy 62 LPNQRTVNVNRGMSLHDCIMKALKVGRLOPECCAVFRLHHEHKGKARLDWNTDAASL 121
Db 161 LPNQRTVWPARGVTVRDSLKKALMMRGLIPECCAVYRI---QDGEKKPIGWDTDISWL 217
Qy 122 IGEELQVDFLDHVLTHNFARKTFLKAPCDICQKFLNGFCQFCGKFEHCSTKYP 181
Db 218 TGEELHVEVLNVPLTHNFVRKTFFTLAFCDFCRKLFLQGFRCQFCGKFKHQRCEVP 277
Qy 182 TMCVDWNSIRQLL-----FPNSTIGDS-GVPALPSLTVR 215
Db 278 LMCVNYDQLDLFLVSKFEHHPISQETTLGETTPAGSYSPVPPSDSVGPPLPS---- 333
Qy 216 RMRESVRMPVSVQHRYSTPHTFTNTSPSSSEGLSQQRQSTPTNVHVMVSTLTPVDSR 275
Db 334 -----PSPSK---SIPQPFPAEDHRNQFQDRSSAPNVH-INTIEPVN-- 378
Qy 276 MIEDAIRSHS-----ESASPSAL----- 293
Db 379 -IDDLIRDOQVRGEGAPLNLMLRKLRYQSTPSPLLHSPSVIFDFEPGVPFRGSTAG 437
Qy 294 -----SSSPNNLSPTGWSQPKTPVPAQRAERAPVSGTQENKLRPRGQDRSSYWIIEAS 347
Db 438 LSATPPASLPGSLTNVAKLQ-KSPGP-QREKSSSSSEDENRKMTLGRDSSDDWELPDG 495
Qy 348 EVMLESTRIGSGSGFTVYKGKHWGDAVKILKVVDPTEPQAPRNEAVLKRTRHVNILL 407
Db 496 QITVGRIIGSGSGFTVYKGKHWGDAVKMLNVNAPTQQLQAPKNEVGVLKRTRHVNILL 555

Qy 408 FMGWTQNTLAIVTQWCEGSSLYKHLHVQETKFFOMFOLIDIARTAGQMDYLHAKNIHR 467
Db 556 FMGISTKPLQALVITQWCEGSSLYHLLHIIETKFFEMIKLIDIARTAGQMDYLHAKSIHR 615
Qy 468 DMKSNNIFLHGLTVKIGDFGLAVTKSRWSGQVQEQPTGSLVWMAPEVIRMDNNPESF 527
Db 616 DLKSNNIFLHGLTVKIGDFGLAVTKSRWSGSHQFEQLSGSILWMAPEVIRMQDKNPISF 675
Qy 528 QSDVYSGIVLYELMTGELPYSHINNRRDQIIFMVGSGYASPDLSKLYKNCPKAMKRLVAD 587
Db 676 QSDVYAFGIVLYELMTGOLPYSNINNRRDQIIFMVGSGYASPDLSKLYKNCPKAMKRLMAE 735
Qy 588 CVKKVKEPRLFPQILSIQLLQHSLSKPKINSASEPSLHRAA-HTEIDN--ACTLTTSR 644
Db 736 CLKKKRDERPLFPQILASIELLARSPLKIHRSASEPSLNRAGFTQEDFSLYAC---ASPK 792
Qy 645 LPV 647
Db 793 TPI 795

RESULT 12
TVWVF6
protein kinase (EC 2.7.1.37) raf - murine sarcoma virus 3611
N:Alternate names: kinase-related transforming protein raf; raf. proto-oncogene protel
C:Species: murine sarcoma virus 3611
A:Note: host Mus musculus (mouse)
C:Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 23-Feb-1997
C:Accession: A00638; A38020
R:Kan, N.C.; Flordellia, C.S.; Mark, G.E.; Duesberg, P.H.; Papas, T.S.
Science 223, 813-816, 1984
A:Title: A common onc gene sequence transduced by avian carcinoma virus MH2 and by mu
A:Reference number: A00638; MUID:84121298; PMID:6320371
A:Accession: A00638
A:Molecule type: DNA
A:Residues: 1-323 <KAN>
A:Experimental source: ATCC 45010
R:Mark, G.E.; Rapp, U.R.
Science 224, 285-289, 1984
A:Title: Primary structure of v-raf: relatedness to the src family of oncogenes.
A:Reference number: A38020; MUID:84172180; PMID:6324342
A:Accession: A38020
A:Molecule type: DNA
A:Residues: 1-323 <MAR>
C:Comment: This protein is translated as a gag-raf polyprotein.
C:Genetics:
A:Gene: raf
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; oncogene; phosphotransferase; serine/threonine-specific protein kina
F:22-288/Domain: protein kinase homology <KIN>
F:30-38/Region: protein kinase ATP-binding motif
F:50/Active site: Lys #status predicted

Query Match 48.5%; Score 1654; DB 1; Length 323;
Best Local Similarity 97.2%; Pred. No. 3.2e-79;
Matches 314; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 326 EKNKTRPRGQDRSSYWIIEASEVMSLSTRIGSGFTVYKGKHWGDAVKILKVVDPTEP 385
Db 1 EKNKTRPRGQDRSSYWIIEASEVMSLSTRIGSGFTVYKGKHWGDAVKILKVVDPTEP 60
Qy 386 QFOAPRNEAVLKRTRHVNILLFMGYMTKDNLAIVTQWCEGSSLYKHLHVQETKFFOMFOL 445
Db 61 QLOAPRNEAVLKRTRHVNILLFMGYMTKDNLAIVTQWCEGSSLYKHLHVQETKFFOMFOL 120
Qy 446 IDIARTAGQMDYLHAKNIHRDKSNNIFLHGLTVKIGDFGLATVKSRSWGSGQVQEQP 505
Db 121 IDIARTAGQMDYLHAKNIHRDKSNNIFLHGLTVKIGDFGLATVKSRSWGSGQVQEQP 180
Qy 506 TGSVLWMAPEVIRMDNNPFSQSDVSYGIVLYELMTGELPYSHINNRRDQIIFMVG 565
Db 181 TGSVLWMAPEVIRMDNNPFSQSDVSYGIVLYELMTGELPYSHINNRRDQIIFMVG 240

QY	566	ASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFPQILSSIELLQHSPLKINSASEPSL	625
Db	241	ASPDLSRLYKNCPKAKRLVADCVKVKKEERPLFPQILSSIELLQHSPLKINSASEPSL	300
QY	626	HRAAHTEDINACTLTSPRLPVF	648
Db	301	HRAAHTEDINACTLTSPRLPVF	323
RESULT 13			
TVMSRP			
protein kinase A-raf-1 (EC 2.7.1.-) - mouse (fragment)			
N:Alternate names: A-raf-1 proto-oncogene protein-serine/threonine kinase; kinase-related			
C:Species: Mus musculus (house mouse)			
C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 11-Jun-1999			
C:Accession: A25382			
R:Huleihel, M.; Goldsborough, M.; Cleveland, J.; Gunnell, M.; Bonner, T.; Rapp, U.R.			
Mol. Cell. Biol. 6, 2655-2662, 1986			
A:Title: Characterization of murine A-raf, a new oncogene related to the v-raf oncogene.			
A:Reference number: A25382; MUID:87064566; PMID:3491291			
A:Accession: A25382			
A:Molecule type: mRNA			
A:Residues: 1-437 <HUL>			
A:Cross-references: GB:M13071; NID:g192016; PIDN:AAA37258.1; PID:g387104			
C:Genetics:			
A:Gene: A-raf			
C:Function:			
A:Description: signal transduction between cell membrane and nucleus; after phosphorylat			
A:Pathway: MAP kinase cascade			
A:Note: in mouse, expressed in urogenital tissues and, at lower levels, in other tissues			
C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; prot			
C:Keywords: Atp; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene			
F:139-405/Domain: protein kinase homology <KIN>			
F:147-195/Region: protein kinase ATP-binding motif			
F:47/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted			
F:56/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted			
F:167/Active site: Lys #status predicted			
F:413/Binding site: phosphate (Ser) (covalent) #status predicted			
Query Match 41.3%; Score 1409.5; DB 1; Length 437;			
Best Local Similarity 66.7%; Pred. No. 2.3e-66;			
Matches 275; Conservative 53; Mismatches 71; Indels 13; Gaps 6;			
QY	243	SSPSSEGLSQORSTSTPNVHMVSTLTPVDSRMIEDAIRSHSESA-----SPSALSS	295
Db	31	SFPAPANPLQLRISTSTPNVHMVSTAPMDSSLMQTAQSFSTDAAGRGDGPARG-SP	89
QY	296	SPNNLSPTGWSQKTPVPA-QREAPVSGTQEKNKIRPGORDSSVYWEIEASEVWLSTR	354
Db	90	SPASVS-SGRKSPHSKLPSPQREKSLA--DEKKYKNLGYRDSGYWEVPPSEVQLKR	146
QY	355	IGSGSFGTVYKKGWGDVAVKILKVDPTPEQFQAFNEVAVLKRTRHVNILLFMGYMK	414
Db	147	IGTSGTVYFGLHWGDVAVKLVKVAQPTAEQAQAKFENQVLRKTRHVNILLFMGFMR	206
QY	415	DNLAIVTQWCCESSLYKHLHVQETKFOFQFOLIDIARTAQGM DYLHAKNIIHDMKSNNI	474
Db	207	PGFALITQWCCESSLYKHLHVADTFDMVQLIDVARTAQGM DYLHAKNIIHDLKSNNI	266
QY	475	FLHGLTVKIGDFGLATVKSNSGSGQVEQPTGSLVMAPEVIRMODNPNPESQSDVSY	534
Db	267	FLHGLTVKIGDFGLATVKTWSGAQPLEQPSGSLVMAAEVIRMODPNPESQSDVYAY	326
QY	535	IGVLYELMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKRE	594
Db	327	GVLYELMTGSLPYSHIGSRDQIIFVMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKRE	386
QY	595	ERPLFPQILSSIELLQHSPLKINSASEPSLHRAAHTEDINACTLTSPRLP	646
Db	387	ERPLFPQILATLQLRSLPKIERSASEPSLHR-TQADLPACLLSARLVP	437
RESULT 14			
S47244			
C:raf protein - zebra fish			
C:Species: Brachydanio rerio (zebra fish)			
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 24-Sep-1999			
C:Accession: S47244			
R:Daniotti, J.L.			
submitted to the EMBL Data Library, August 1994			
A:Reference number: S47244			
A:Accession: S47244			
A>Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-307 <DAN>			
A:Cross-references: EMBL:X81128; NID:g534976; PIDN:CAA57035.1; PID:g534977			
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom			
C:Keywords: Atp			
F:7-273/Domain: protein kinase homology <KIN>			
F:15-23/Region: protein kinase ATP-binding motif			
Query Match 41.0%; Score 1398.5; DB 2; Length 307;			
Best Local Similarity 88.1%; Pred. No. 5.8e-66;			
Matches 266; Conservative 20; Mismatches 15; Indels 1; Gaps 1;			
QY	347	SEVMLSTRIGSGSGFTVYKKGWGDVAVKILKVDPTPEQFQAFNEVAVLKRTRHVNIL	406
Db	7	NEVLSRLGSGSGFTVYKKGWGDVAVKLVKVTNPTEQFQAFNEVAVLKRTRHVNIL	66
QY	407	LFMGYMTKDNLAIVTQWCCESSLYKHLHVQETKFOFQFOLIDIARTAQGM DYLHAKNIIH	466
Db	67	LFMGYMTKGNLAIVTQWCCESSLYKHLHVLETFQFQFOLIDIARTAQGM DYLYMKRHH	126
QY	467	RDMSNNIFLHGLTVKIGDFGLATVKSNSGSGQVEQPTGSLVMAPEVIRMODNPNPES	526
Db	127	RDMSNNIFLHGLTVKIGDFGLATVKAWSGSGQVEQPSGSLVMAPEVIRMQDNNPYS	186
QY	527	FQSDVYSYGVLYELMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPKAMKRLVA	586
Db	187	FQSDVYSYGVLYELMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPKAMKRLVA	246
QY	587	DCVKKVKEERPLFPQILSSIELLQHSPLKINSASEPSLHRAAHTEDINACTLTSPRLP	646
Db	247	DCIKSKDERPLFPQILSSIELLQHSPLKINSASEPSLHRAASQSDISSCTL-TSMKLP	305
QY	647	VF 648	
Db	306	VF 307	
RESULT 15			
TVFFDF			
protein kinase Draf-1 (EC 2.7.1.-) - fruit fly (Drosophila melanogaster)			
N:Alternate names: Draf-1 proto-oncogene protein-serine/threonine kinase; kinase-rela			
C:Species: Drosophila melanogaster			
C>Date: 31-Mar-1991 #sequence_revision 23-Feb-1996 #text_change 23-Feb-1997			
C:Accession: S00393; S60191; A27808; S33602			
R:Nishida, Y.; Hata, M.; Ayaki, T.; Ryo, H.; Yamagata, M.; Shimizu, K.; Nishizuka, Y.			
EMBO J. 7, 775-781, 1988			
A:Title: Proliferation of both somatic and germ cells is affected in the Drosophila m			
A:Reference number: S00393; MUID:88283647; PMID:3135183			
A:Accession: S00393			
A:Molecule type: DNA			
A:Residues: 1-781 <NIS>			
A:Cross-references: EMBL:X07181			
A:Note: the assignment of the start codon has been revised in reference S33602			
A:Accession: S60191			
A:Molecule type: mRNA			
A:Residues: 148-781 <NIS2>			
R:Mark, G.E.; MacIntyre, R.J.; Digan, M.E.; Ambrosio, L.; Perrimon, N.			
Mol. Cell. Biol. 7, 2134-2140, 1987			
A:Title: Drosophila melanogaster homologs of the raf oncogene.			
A:Reference number: A27808; MUID:87257926; PMID:3037346			
A:Accession: A27808			
A:Molecule type: mRNA			
A:Residues: 'LQ', 465-519, 'R', 521, 'A', 523-570, 'R', 572-699, 'PQAL', 704-713, 'PT', 716-753			

R; Sprenger, F.; Troscclair, M.M.; Morrison, D.K.
Mol. Cell. Biol. 13, 1163-1172, 1993
A: Title: Biochemical analysis of torso and D-raf during Drosophila embryogenesis: implic
A: Reference number: S33602; MUID: 93140754; PMID: 8423783
A: Contents: annotation
A: Note: this is a revision of the assignment of the start codon in reference S00393
A: Note: the authors call the N-terminal extended version of the protein Draf-3
A: Note: the cited sequence in S33602 shows Pro for residue 342
C: Genetics:
A: Gene: Draf-1
A: Cross-references: FlyBase: FBgn0003079
A: Map position: X 2F
A: Introns: 417/3; 464/3; 589/2
C: Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; prot
C: Keywords: ATP; phosphotransferase; proto-oncogene; serine/threonine-specific protein k
F: 265-310/Domain: protein kinase C zinc-binding repeat homology <K22>
F: 469-735/Domain: protein kinase homology <KIN>
F: 477-485/Region: protein kinase ATP-binding motif
F: 497/Active site: Lys #status predicted

Query Match 40.0%; Score 1365; DB 1; Length 781;
Best Local Similarity 46.4%; Pred. NO. 9.2e-64;
Matches 304; Conservative 86; Mismatches 193; Indels 72; Gaps 16;

QY 32 IVQFGYORRASDDGKLT-----PSKTSNT-----IRVFLPNKQRTVYVVRNMSL 78
DB 146 ILQOQRLARVHHGTDLDSLGSPGSCGTLTQPKILLRAHLPNQORTSVEVISGRL 205
QY 79 HDCLMKALKVGLQPECAVRLLEHKKARLDWNTDAASLIGEELQVDFLDHVLPTT 138
DB 206 CDALMKALKRLQTPDMCEVST---THSGRHI-IPWHTDITGLHVEIFVRLLDKFPRT 261
QY 139 ---HNFARKTEFLKAFCDICQKELLNGFRCTCYKKEHCSTKVPVPCVDM--SNIRQL 193
DB 262 HIKHQLINKTFSLVFCGECRLFTGYCSQCNEFRHQRANRVPMLCQPPMDSYQL 321
QY 194 LIFNSTIGSGVPALPSLMMRRESVSRMPVSSQHRYSYTHAFNTSS---PSSEGS- 250
DB 322 LLAENP---DNGV-GFPG-----RGTAVERNSSRSRRCSSGSSSSSKPPSSSGN 371
QY 251 -----LSQRORSTSPNV---HMVSTLPVDSDMIEDA-----IRSHSESASPSA 292
DB 372 HRQRPPIRISQDDKSNAPNCININRSVTSEVQSLIMOARPPPLPHPCPTDHSNSTQASP 431
QY 293 LSSSPNNLPTGWSQKPTVPVPAQRERAPVSGTQKKNKIRPGORDSSYYWEIEASEVMLS 352
DB 432 TSTLKH-----RPRARSADESNKLL--RDAKSEENWNILAEELIG 474
QY 353 TRIGSGSGVYVYKKGHDVAVKILKVVDTPPEQFAFRNEVAVLRKTRHVNILLFMGYM 412
DB 475 PRIGSGSGVYVYRAHWPVAVKTLNVKTPSPAQLQAFKNEVAMLKTRHCNILLFMGCV 534
QY 413 TKDNLAIQTQWCGSSLYKHLHYQETKFMOLFIDTARQTQAGMDYLHAKNIHRDMKSN 472
DB 535 SKPSLAIVTQWCGSSLYKHVHVSEYKFKLNTLIDIGRVAQGMDFHAKNIHRDLKSN 594
QY 473 NIFLHGLTVKIGDFGLATVKWSGSQQVEQPTGSVLWMAPEVIRMQDNNPFSQSDVY 532
DB 595 NIFLHEDLSYKIGDFGLATVAKTRWGEKQANQPTGSILWMAPEVIRMQELNPFQSDVY 654
QY 533 SYGIVLYELMTGELPYSHINRDQIIFMVGRYASPDLSKLYKNCPKAMKRLVADCVKRY 592
DB 655 AFGIVMYELLAECPLPYGHISNKKDQILFMVGRLLPDMDSQVRSDDARRHKKRAEDCIKYT 714
QY 593 KEERPLFPQILSLIHLQSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRPV 647
DB 715 PKDRPLRPLNMLNMLRTLPKIHRSASEPNLTQSQOND---EFLYLPSPKTPV 767

Search completed: July 9, 2003, 09:46:42
Job time : 25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: July 9, 2003, 09:46:18 ; Search time 28 Seconds
(without alignments)
2694.286 Million cell updates/sec

Title: US-09-637-302C-2
Perfect score: 3413
Sequence: 1 MEHIQGAWKTTISNGFGFKDA.....AHTEDINACTLTTSPLPVPF 648

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep.*
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 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3413	100.0	648	9	US-09-513-145-6
2	3413	100.0	648	9	US-10-059-585-38
3	1891.5	55.4	604	9	US-10-205-342-1
4	1165	34.1	271	10	US-09-840-704-6
5	1143	33.5	217	9	US-09-513-145-5
6	786	23.0	148	9	US-09-513-145-4
7	646	18.9	125	10	US-09-925-302-849
8	457.5	13.4	850	10	US-09-904-389-2
9	422.5	12.4	263	10	US-09-840-704-5
10	404	11.8	505	9	US-09-977-260-6
11	404	11.8	505	9	US-09-977-261-6
12	404	11.8	505	10	US-09-977-269-6
13	404	11.8	505	10	US-09-982-610-20
14	403	11.8	537	9	US-09-977-260-11
15	403	11.8	537	9	US-09-977-261-11
16	403	11.8	537	10	US-09-977-269-11
17	400	11.7	537	10	US-09-771-161A-212
18	400	11.7	537	10	US-09-771-161A-213
19	397	11.6	536	9	US-09-977-260-13

20	397	11.6	536	9	US-09-929-266-10	Sequence 10, Appl
21	397	11.6	536	9	US-09-977-261-13	Sequence 13, Appl
22	397	11.6	536	10	US-09-977-269-13	Sequence 13, Appl
23	395	11.6	543	9	US-09-977-260-14	Sequence 14, Appl
24	395	11.6	543	9	US-09-977-261-14	Sequence 14, Appl
25	395	11.6	543	10	US-09-977-269-14	Sequence 14, Appl
26	391.5	11.5	983	9	US-10-205-823-97	Sequence 97, Appl
27	391.5	11.5	983	10	US-09-771-161A-227	Sequence 227, Appl
28	388	11.4	536	9	US-09-977-260-12	Sequence 12, Appl
29	388	11.4	536	9	US-09-977-261-12	Sequence 12, Appl
30	388	11.4	536	10	US-09-977-269-12	Sequence 12, Appl
31	382	11.2	256	10	US-09-840-704-4	Sequence 4, Appl
32	380.5	11.1	257	9	US-09-823-187-46	Sequence 46, Appl
33	379	11.1	512	9	US-09-977-260-16	Sequence 16, Appl
34	379	11.1	512	9	US-09-977-261-16	Sequence 16, Appl
35	379	11.1	512	10	US-09-977-269-16	Sequence 16, Appl
36	379	11.1	991	9	US-09-823-187-44	Sequence 44, Appl
37	378.5	11.1	859	9	US-10-153-668-324	Sequence 324, App
38	373	10.9	425	10	US-09-828-313-29	Sequence 29, Appl
39	373	10.9	746	9	US-10-153-668-436	Sequence 436, App
40	373	10.9	892	9	US-10-153-668-438	Sequence 438, App
41	371	10.9	509	9	US-09-977-260-18	Sequence 18, Appl
42	371	10.9	509	9	US-09-977-261-18	Sequence 18, Appl
43	371	10.9	509	10	US-09-977-269-18	Sequence 18, Appl
44	370.5	10.9	928	8	US-08-578-684-2	Sequence 2, Appl
45	370.5	10.9	1276	10	US-09-982-610-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-513-145-6
; Sequence 6, Application US/09513145
; Publication No. US20030192723A1
; GENERAL INFORMATION:
; APPLICANT: Yoo, Tai-June
; TITLE OF INVENTION: Antigen to Systemic Lupus Erythematositis and Diagnostic
; FILE REFERENCE: 2502-1-2
; CURRENT APPLICATION NUMBER: US/09/513,145
; CURRENT FILING DATE: 2000-02-25
; EARLIER APPLICATION NUMBER: 60/121548
; EARLIER FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-145-6

Query Match	100.0%	Score 3413;	DB 9;	Length 648;
Best Local Similarity	100.0%	Pred. No. 2.6e-246;		
Matches 648;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MEHIQGAWKTTISNGFGFKDAVFDGSSCISPTIVQFGYQRRASDDGKLTDPKSTNIRV	60	
Db	1	MEHIQGAWKTTISNGFGFKDAVFDGSSCISPTIVQFGYQRRASDDGKLTDPKSTNIRV	60	
QY	61	FLPNKQRTVVNVRNGSLHDCLMKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAAS	120	
Db	61	FLPNKQRTVVNVRNGSLHDCLMKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAAS	120	
QY	121	LIGEEQVDFLDHVPVLTTHNFARKTKLAFCDICOKFLLNGPRCOTCCYKKEHCSTKV	180	
Db	121	LIGEEQVDFLDHVPVLTTHNFARKTKLAFCDICOKFLLNGPRCOTCCYKKEHCSTKV	180	
QY	181	PTMCVDWSNIRQLLLFPNSTIGDSVGPALPSTLMRRRESVSMPYSSQHRYSTPHATTF	240	
Db	181	PTMCVDWSNIRQLLLFPNSTIGDSVGPALPSTLMRRRESVSMPYSSQHRYSTPHATTF	240	
QY	241	NTSSPSEGLSQORSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSPNNL	300	

Db 241 NTSSPSEGLSQRSTSTPNVHMVSTTLPLVDNRMIEDAIRSHSESASPALSPPNNL 300
Qy 301 SPTGWSQPKTPVPAQRERAPVSTQEKNIIRPRGORDSSYYWEIEASEVYMLSTRIGSGSF 360
Db 301 SPTGWSQPKTPVPAQRERAPVSTQEKNIIRPRGORDSSYYWEIEASEVYMLSTRIGSGSF 360
Qy 361 GTVYKGKWHGDVAVKILKVVDPPTPEQFAFRNEVAVLRKTRHVNILLFMYMTKDNLAIV 420
Db 361 GTVYKGKWHGDVAVKILKVVDPPTPEQFAFRNEVAVLRKTRHVNILLFMYMTKDNLAIV 420
Qy 421 TQWCEGSSLYKHLHVQETKFMQFOLIDIARQTAQGMVYLRHAKNIIRHDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKFMQFOLIDIARQTAQGMVYLRHAKNIIRHDMKSNIFLHEGL 480
Qy 481 TVKIGDFGLATVKSRSWGSQOQVPTGSLVMAPEVIRMQDNNPFSQSDVYSYGVLYE 540
Db 481 TVKIGDFGLATVKSRSWGSQOQVPTGSLVMAPEVIRMQDNNPFSQSDVYSYGVLYE 540
Qy 541 LMTGELPYSHINNRDQIIFMVGRGYASPDLSKLYKNCPCAMKRLVADCVKVKKEERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFMVGRGYASPDLSKLYKNCPCAMKRLVADCVKVKKEERPLFP 600
Qy 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 2

US-10-059-585-38
; Sequence 38, Application US/10059585
; Publication No. US20030082776A1
; GENERAL INFORMATION:
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/059,585
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 100.0%; Score 3413; DB 9; Length 648;
US-10-059-585-38

Best Local Similarity 100.0%; Pred. No. 2.6e-246;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEHIQGAWKTTISNGFGFKDAVDFDGGSSCISPTIVQFGVQRRASDDGKLTDPSTKTSNTIRV 60
Db 1 MEHIQGAWKTTISNGFGFKDAVDFDGGSSCISPTIVQFGVQRRASDDGKLTDPSTKTSNTIRV 60
Qy 61 FLPNKQRTVVNVNRGMSLHDCIMKALKVIRGLQPECCAVFRLHHEHKGKARLDWNTDAAS 120
Db 61 FLPNKQRTVVNVNRGMSLHDCIMKALKVIRGLQPECCAVFRLHHEHKGKARLDWNTDAAS 120
Qy 121 LIGBELQVDFLDHVPPLTHNFARKYFLKAPDCICQKFLNGFRQCQCGKFKFHEHCSTKV 180
Db 121 LIGBELQVDFLDHVPPLTHNFARKYFLKAPDCICQKFLNGFRQCQCGKFKFHEHCSTKV 180
Qy 181 PTMCVDNSNIHQLLFPNSTIGDSVPALPSLTWRRKRESVSRMPVSSQHRISTPHTFTF 240
Db 181 PTMCVDNSNIHQLLFPNSTIGDSVPALPSLTWRRKRESVSRMPVSSQHRISTPHTFTF 240
Qy 241 NTSSPSEGLSQRSTSTPNVHMVSTTLPLVDNRMIEDAIRSHSESASPALSPPNNL 300
Db 241 NTSSPSEGLSQRSTSTPNVHMVSTTLPLVDNRMIEDAIRSHSESASPALSPPNNL 300
Qy 301 SPTGWSQPKTPVPAQRERAPVSTQEKNIIRPRGORDSSYYWEIEASEVYMLSTRIGSGSF 360
Db 301 SPTGWSQPKTPVPAQRERAPVSTQEKNIIRPRGORDSSYYWEIEASEVYMLSTRIGSGSF 360
Qy 361 GTVYKGKWHGDVAVKILKVVDPPTPEQFAFRNEVAVLRKTRHVNILLFMYMTKDNLAIV 420
Db 361 GTVYKGKWHGDVAVKILKVVDPPTPEQFAFRNEVAVLRKTRHVNILLFMYMTKDNLAIV 420
Qy 421 TQWCEGSSLYKHLHVQETKFMQFOLIDIARQTAQGMVYLRHAKNIIRHDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKFMQFOLIDIARQTAQGMVYLRHAKNIIRHDMKSNIFLHEGL 480
Qy 481 TVKIGDFGLATVKSRSWGSQOQVPTGSLVMAPEVIRMQDNNPFSQSDVYSYGVLYE 540
Db 481 TVKIGDFGLATVKSRSWGSQOQVPTGSLVMAPEVIRMQDNNPFSQSDVYSYGVLYE 540
Qy 541 LMTGELPYSHINNRDQIIFMVGRGYASPDLSKLYKNCPCAMKRLVADCVKVKKEERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFMVGRGYASPDLSKLYKNCPCAMKRLVADCVKVKKEERPLFP 600
Qy 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 3

US-10-205-342-1
; Sequence 1, Application US/10205342
; Publication No. US20030108906A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018198
; CURRENT APPLICATION NUMBER: US/10/205,342
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: A-raf protein (AA 1-604)
US-10-205-342-1

```
Query Match      55.4%; Score 1891.5; DB 9; Length 604;
Best Local Similarity 61.7%; Pred. No. 7.2e-133;
Matches 377; Conservative 76; Mismatches 125; Indels 33; Gaps 10;

QY 50 DPSKTSNTIRVFLPNKORTVVVNGSLHDLCKALKVKGRLQPECCAVFLLHEHKGKK 109
DB 13 EPSRAVGTVKVLNPKORTVVVTRDGMVSDSLDKALKVRLGNQDCCVYRLI---KGRK 69

QY 110 ARLDNMTDAASLIGEEQLQVDFLDHVPLTTHNFARKTFELKLAFCDCIKOKELLNPFRCOTCG 169
DB 70 TVTAWDAIAPLDGEELIVELEDVPLTMNFKYKTFEFLAFCDLFLFHGFRCTCG 129

QY 170 YKFEHGSTKPTMCVDMWS-NIROLLEFPNSTIGSGVPALPSLTMRMRESVSRMPVSS 228
DB 130 YKPHGCHSSKPTVCVDMSTNRQFYHSIQDLGGSS-----RQCEVPSNLSVNE 178

QY 229 QHRYSTPHAF-----FNTSSPSEGLSORQSTSTPNVHMVSTLTPVDSRMIEDAIRS 283
DB 179 LLTPQSPPTQQRDQEHFEPAPANPLQRIKIRSTSTPNVHMVSTTAPMDSSLMQFTAQS 238

QY 284 HSESA-----SPSALSSSPNNLSPTGWSQKPTVPA-QRERAPVSGTGKKNIRPRGQ 335
DB 239 FSTDAAGRGGDGAPRG-SPSPASVS-SGRKSPHSKLPACQERKSLA--DEKKVKNLGY 294

QY 336 RDSYYWEIEASEVMLSTRIGSGSGFGTVYKKGWGDVAVKILKVVDPTPQFOAFRNEVA 395
DB 295 RDSYYWEVPPSEVQLLRIGTSGFGTVFRGRHGDVAVKLVKAQPTAEQAQAFKNEMQ 354

QY 396 VLKTRHVNILLFGYMTKONLAIVTQWCEGSSLYKHLHVOETKFMQLIDTAROTAG 455
DB 355 VLKTRHVNILLFGWFTRGFEALITQWCEGSSLYHHLHVADRFDMVQLIDVAROTAG 414

QY 456 MDYLHAKNIHRLDKSNIFLHGLTVKIGDFGLATVKSRWSGQVQPTGSLVMAPE 515
DB 415 MDYLHAKNIHRLDKSNIFLHGLTVKIGDFGLATVKSRWSGQVQPTGSLVMAAE 474

QY 516 VIRMQDNPFSDVSYGIVLYELMTGELPYSHINNRDQIIFWVGRGYASPDLSKLYK 575
DB 475 VIRMQDNPFSDVSYGIVLYELMTGELPYSHINNRDQIIFWVGRGYASPDLSKLYK 534

QY 576 NCPKAMRLVADVCKYKERPLFPQILSSIELLQHSPLKINRSASEPSLHRAAHTEDIN 635
DB 535 NCPKAMRLVADVCKYKERPLFPQILSSIELLQHSPLKINRSASEPSLHRAAHTEDIN 593

QY 636 ACTLTSPLRP 646
DB 594 ACLLSAARLVP 604
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RESULT 4
US-09-840-704-6
; Sequence 6, Application US/09840704
; Patent No. US20020122801A1
; GENERAL INFORMATION:
; APPLICANT: Dedhar, Shoukat
; APPLICANT: Hannigan, Greg
; TITLE OF INVENTION: Intergrin-Linked Kinase and its Uses
; FILE REFERENCE: KIN-2CON
; CURRENT APPLICATION NUMBER: US/09/840,704
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/566,906
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US08/752,345
; PRIOR FILING DATE: 1996-11-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 271
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
```

```
; LOCATION: (1)....(271)
US-09-840-704-6

Query Match      34.1%; Score 1165; DB 10; Length 271;
Best Local Similarity 80.4%; Pred. No. 3.8e-79;
Matches 218; Conservative 25; Mismatches 28; Indels 0; Gaps 0;

QY 344 IEASEVMLSTRIGSGSGFGTVYKKGWGDVAVKILKVVDPTPQFOAFRNEVAVLRKTRHV 403
DB 1 IPDQITVQORIGSGSGFGTVYKKGWGDVAVKILKVVDPTPQLOAFKNEVGLRKRTRHV 60

QY 404 NILLEFGYMTKONLAIVTQWCEGSSLYKHLHVOETKFMQLIDTAROTAGMDYLHAKN 463
DB 61 NILLEFGYMTKONLAIVTQWCEGSSLYHHLHIEKFMKILIDTAROTAGMDYLHAKS 120

QY 464 IHRDKSNIFLHGLTVKIGDFGLATVKSRWSGQVQPTGSLVMAPEVIRMQDN 523
DB 121 IHRDKSNIFLHGLTVKIGDFGLATVKSRWSGSHQEQLSGSLMMAPEVIRMQDN 180

QY 524 PFSFQSDVSYGIVLYELMTGELPYSHINNRDQIIFWVGRGYASPDLSKLYKNCPKAMKR 583
DB 181 PFSFQSDVSYGIVLYELMTGELPYSHINNRDQIIFWVGRGYASPDLSKLYKNCPKAMKR 240

QY 584 LVADVCKYKERPLFPQILSSIELLQHSPL 614
DB 241 LMAECLKKRDERPLFPQILASSIELLARSPL 271

RESULT 5
US-09-513-145-5
; Sequence 5, Application US/09513145
; Publication No. US20020192723A1
; GENERAL INFORMATION:
; APPLICANT: Yoo, Tai-June
; TITLE OF INVENTION: Antigen to Systemic Lupus Erythematosus and Diagnostic
; FILE REFERENCE: 2502-1-2
; CURRENT APPLICATION NUMBER: US/09/513,145
; CURRENT FILING DATE: 2000-02-25
; EARLIER APPLICATION NUMBER: 60/121548
; EARLIER FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-513-145-5

Query Match      33.5%; Score 1143; DB 9; Length 217;
Best Local Similarity 100.0%; Pred. No. 1.2e-77;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 GFCOTCGYKFEHCSTKVPKVCVDWNSNIROLLEFPNSTIGSGVPALPSLTMRMRESV 221
DB 1 GFCOTCGYKFEHCSTKVPKVCVDWNSNIROLLEFPNSTIGSGVPALPSLTMRMRESV 60

QY 222 SRMPVSSQHRYSTPHAFTFNTSSPSEGLSQORQSTSTPNVHMVSTLTPVDSRMIEDAI 281
DB 61 SRMPVSSQHRYSTPHAFTFNTSSPSEGLSQORQSTSTPNVHMVSTLTPVDSRMIEDAI 120

QY 282 RSHSESASPSALSSPNLSPTGWSQKPTVPAQRERAPVSGTGKKNIRPRGQDSSYY 341
DB 121 RSHSESASPSALSSPNLSPTGWSQKPTVPAQRERAPVSGTGKKNIRPRGQDSSYY 180

QY 342 WEIEASEVMLSTRIGSGSGFGTVYKKGWGDVAVKILK 378
DB 181 WEIEASEVMLSTRIGSGSGFGTVYKKGWGDVAVKILK 217

RESULT 6
US-09-513-145-4
; Sequence 4, Application US/09513145
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; Publication No. US20020192723A1
; GENERAL INFORMATION:
; APPLICANT: Yoo, Tai-June
; TITLE OF INVENTION: Antigen to Systemic Lupus Erythematosus and Diagnostic
; FILE REFERENCE: 2502-1-2
; CURRENT APPLICATION NUMBER: US/09/513,145
; CURRENT FILING DATE: 2000-02-25
; EARLIER APPLICATION NUMBER: 60/121548
; EARLIER FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-145-4

Query Match      23.0%; Score 786; DB 9; Length 148;
Best Local Similarity 100.0%; Pred. No. 3.1e-51;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTQAWKTSISNGFGKDAVFGSSCISPTIIVQFGYQRRASDDGKLTDPKTSNTIRV 60
DB 1 MEHTQAWKTSISNGFGKDAVFGSSCISPTIIVQFGYQRRASDDGKLTDPKTSNTIRV 60

QY 61 FLPNKQRTVVNRGMSLHDLCKALKVRLQPECCAVFLLHEHKGKRLDWNNTDAAS 120
DB 61 FLPNKQRTVVNRGMSLHDLCKALKVRLQPECCAVFLLHEHKGKRLDWNNTDAAS 120

QY 121 LIGELQVDFLDHVPPLTHNFARKTFLK 148
DB 121 LIGELQVDFLDHVPPLTHNFARKTFLK 148

RESULT 7
US-09-925-302-849
; Sequence 849, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 849
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (113)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (116)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (118)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (125)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-849

Query Match      18.9%; Score 646; DB 10; Length 125;
Best Local Similarity 96.8%; Pred. No. 6.9e-41;
Matches 120; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

; Publication No. US2002012940A1
; GENERAL INFORMATION:
; APPLICANT: Clendennen, Stephanie K.
; TITLE OF INVENTION: CTRL HOMOLOGUE FROM MELON
; FILE REFERENCE: 4257-0029.30
; CURRENT APPLICATION NUMBER: US/09/904,389
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/218,307
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 850
; TYPE: PRT
; ORGANISM: Cucumis melo
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (154)...(154)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-904-389-2

Query Match      13.4%; Score 457.5; DB 10; Length 850;
Best Local Similarity 35.3%; Pred. No. 1e-25;
Matches 125; Conservative 68; Mismatches 116; Indels 45; Gaps 14;

QY 288 ASPSALSSSP-----NNLSPTGWSQPKTPVPAQRERAP-----VSGTQ--EKNKI 330
DB 503 ASFYVQSTPFVENVVPLSHISHISESEHLLALSHPRMDHVNLLPFVHGSOLIRKPYNE 562
QY 331 RPRGQRDSSYYWEIEASEVYMLSTRIGSGFVYKKGWHG-DVAVKILKVVDPDPEQFOA 389
DB 563 LSLGLEDLVIPW----TDLDLREKIGAGSGFTYRGEGWHGSDVAVKILTEQDFHPYRNE 618
QY 390 FRNEVAVLRKTRHVNILLFWGYTK-DNLAIYTORCEGSSLYKHLH-----VQETKQOM 442
DB 619 FLREVAIMKSLRHPNIVLFWGAVTTPPNLSIVTELSRGSLLRLLHKGSGVKDIDETR--- 675
QY 443 FQIDILAROTACOMDYLHAKN--IIHRDMKSNIFLHEGLTVKIGDFGLATVKSWSGQ 500
DB 676 --RINAFDVAKGMVYLRHDPPIVHRDLKSNLLVDKRYTVKVCDFGLSRKARTELSS 733
QY 501 QVEQPTGSLVMAPEVIRMODNNPFSQSDVTSYGIVLYELMTGELPYSHINNRQIIFM 560
DB 734 --KSAAGTPEWNAPEVLR---DEPSNEKSDVTSYFVILWELATLQOPMCNLNPA-QVVA 787
QY 561 VGRGYASPDLSKLYKNCPRKMKELVADCVKVKKEERPLFPQILSSITLLOHSLP 614
DB 788 VGFGRKRLDIPRDN--PKLASLIVA-CWADEPWKRPSFSSIMETLKPMTKQAP 838

RESULT 9
US-09-840-704-5
; Sequence 5, Application US/09840704
; Patent No. US20020122801A1
; GENERAL INFORMATION:
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; APPLICANT: Dedhar, Shoukat
; APPLICANT: Hannigan, Greg
; TITLE OF INVENTION: Intergrin-Linked Kinase and its Uses
; FILE REFERENCE: KIN-200N
; CURRENT APPLICATION NUMBER: US/09/840,704
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/566,906
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US08/752,345
; PRIOR FILING DATE: 1996-11-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 263
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (1)...(263)
US-09-840-704-5

Query Match      12.4%; Score 422.5; DB 10; Length 263;
Best Local Similarity 37.3%; Pred. No. 8.6e-24;
Matches 100; Conservative 63; Mismatches 90; Indels 15; Gaps 9;

QY 348 EVMLSTRIGSGFTVYKKGWHG--DVAVKILKVVDPPEQFAFRNEVAVLKRTHVNL 406
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 DLNIKEIKGAGSGFTVHRAEWHGSDVAVKILMEQDFHAERVNEFLREVAIMKRLRHPNIV 64

QY 407 LFMGYMK-DNLAIVTQWCESSLYKHLHVQETQFQFQ--LIDIAQTAGMDYLHAKN 463
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 65 LFMGAVTQPPNLSITYETLSRGLYRLHLKSGAREQLDERRRLSMAYDVAKGMNLYHN 124

QY 464 --IHRDMKSNIFLHEGLTVKIGDFGLATVKSWSGSQOQVEOPTGSVLWMAPEVIRMQD 521
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 125 PPIVHRDLKSNLNVDRKTYVKVCDGLSLRKA--SFLSKSAGTPEWMAPEVLR-- 179

QY 522 NNPSFQSDVYSYGIVLYELMTGELPYSHINNRDQIIFMVGGRGYASPDLSKLYKNCPKAM 581
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 180 DEPSNEKSDVYSFGVILWELATLQPPWGNLPA-QVVAAV--GPKCKRL-EIPRNLNPQV 235

QY 582 KRLVADCVKKEERPLFPQILSSIELL 609
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 236 AAIIEGWTNPEWKRPSFATIMDLRLPL 263

RESULT 10
US-09-977-260-6
; Sequence 6, Application US/09977260
; Publication No. US20020192790A1
; GENERAL INFORMATION:
; APPLICANT: ULLRICH, AXEL
; APPLICANT: GISHIZKY, MIKHAIL
; APPLICANT: SURES, IRMINGARD
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1260
; CURRENT APPLICATION NUMBER: US/09/977,260
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 08/232,545
; PRIOR FILING DATE: 1994-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Megakaryocyte
; OTHER INFORMATION: kinase 3
US-09-977-260-6

Query Match      11.8%; Score 404; DB 9; Length 505;
Best Local Similarity 34.1%; Pred. No. 4.9e-22;
Matches 100; Conservative 55; Mismatches 110; Indels 28; Gaps 11;

QY 329 KIRPGORDSSY----YWEIEASEVNLSTRIGSGFTVYKKGWHG--DVAVKILKVVDP 382
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 210 KIQVPAPFDLSYKTVQDWEIDRNSIQLLKRLSGSGQGEVWEGWLNNTTPVAVKTLKPGSM 269

QY 383 TPQFOAFRNEVAVLKRTHVNLFLPMGYMT-KDNLAIVTQWCESSLYKHLHVQE-TKF 440
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 270 DPND---FLREAQIMKNLRHPKLIQLYAVCTLEDPIYIITELMRHGSQLEQLQNDTGSKI 326

QY 441 QMFQIDIAQTAGMDYLHAKNIHRDMKSNIFLHEGLTVKIGDFGLATV-----KSR 495
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 327 HLTQQVDMAAQVAGSMAYLESRNYIHRDLAARNVLVGEHNTYKVADEGLARVFKVDNEDI 386

QY 496 WSGSQOQVEOPTGSVLWMAPEVIRMQDNNPFSQSDVYSYGIVLYELMT-GELPYSHINNR 554
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 387 YESRHEIKLP---VKWTAPEAIR---SNKFSIKSDVWSFGILLIYIITYGKMPYSGMTGA 440

QY 555 DQIIFWVGGRGYASPDLSKLYKNCPKAMKRLVADCVKKEERPLFPQILSSIE 607
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 441 -QVIQMLAQNYRLPQPS-----NCPQOQFYNIMLECNWNAEPKERTFTETLAWKLE 488

RESULT 11
US-09-977-261-6
; Sequence 6, Application US/09977261
; Publication No. US20030054527A1
; GENERAL INFORMATION:
; APPLICANT: ULLRICH, AXEL
; APPLICANT: GISHIZKY, MIKHAIL
; APPLICANT: SURES, IRMINGARD
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1259
; CURRENT APPLICATION NUMBER: US/09/977,261
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 08/232,545
; PRIOR FILING DATE: 1994-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Megakaryocyte
; OTHER INFORMATION: kinase 3
US-09-977-261-6

Query Match      11.8%; Score 404; DB 9; Length 505;
Best Local Similarity 34.1%; Pred. No. 4.9e-22;
Matches 100; Conservative 55; Mismatches 110; Indels 28; Gaps 11;

QY 329 KIRPGORDSSY----YWEIEASEVNLSTRIGSGFTVYKKGWHG--DVAVKILKVVDP 382
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 210 KIQVPAPFDLSYKTVQDWEIDRNSIQLLKRLSGSGQGEVWEGWLNNTTPVAVKTLKPGSM 269

QY 383 TPQFOAFRNEVAVLKRTHVNLFLPMGYMT-KDNLAIVTQWCESSLYKHLHVQE-TKF 440
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 270 DPND---FLREAQIMKNLRHPKLIQLYAVCTLEDPIYIITELMRHGSQLEQLQNDTGSKI 326

QY 441 QMFQIDIAQTAGMDYLHAKNIHRDMKSNIFLHEGLTVKIGDFGLATV-----KSR 495
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 327 HLTQQVDMAAQVAGSMAYLESRNYIHRDLAARNVLVGEHNTYKVADEGLARVFKVDNEDI 386

QY 496 WSGSQOQVEOPTGSVLWMAPEVIRMQDNNPFSQSDVYSYGIVLYELMT-GELPYSHINNR 554
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 387 YESRHEIKLP---VKWTAPEAIR---SNKFSIKSDVWSFGILLIYIITYGKMPYSGMTGA 440

QY 555 DQIIFWVGGRGYASPDLSKLYKNCPKAMKRLVADCVKKEERPLFPQILSSIE 607
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 441 -QVIQMLAQNYRLPQPS-----NCPQOQFYNIMLECNWNAEPKERTFTETLAWKLE 488
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US-09-977-260-11

Query Match 11.8%; Score 403; DB 9; Length 537;
Best Local Similarity 35.7%; Pred. No. 6.3e-22;
Matches 97: Conservative 55. Mismatches 100. Indels

[illegible]

RESULT 15

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US-09-977-261-11
; Sequence 11, Application US/09977261
; Publication No. US20030054527A1
; GENERAL INFORMATION:
;
; APPLICANT: ULLRICH, AXEL
; APPLICANT: GISHIZKY, MIKHAIL
; APPLICANT: SURES, IRMINGARD
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1259
; CURRENT APPLICATION NUMBER: US/09/977,261
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 08/232,545
; PRIOR FILING DATE: 1994-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-261-11

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Query Match	11.8%	Score	403;	DB	9;	Length	537;
Best Local Similarity	35.7%;	Pred. No.	6.3e-22;				
Matches	97;	Conservative	55;	Mismatches	100;	Indels	20;
						Gaps	19;
QY	342	WEIEASEFVNLSTRGSGSFVTYVKGWKHD--	VAVKILKVDPDTP	EQQAFNEVAVLR	399		
DB	264	WEIPRESQLIKRLNGQGFGEVMTGWNGTKVATIKLP	PGTMSPE---SFELEAQIMKK	320			
QY	400	TRHVNVILLFMGYMTKDNLAIVTQWCEGSSLYKHLHVQETK-FQMQLDI	DIARQTAQGM	458			
DB	321	LKHKDLVOLYAVVSEEPYIVTYEYMNKGSLLDFDKDGEGRALKPLN	LVDMAAQVAA	380			
QY	459	LHAKNIIHRDMKSNPIFHEGLVAVKIGDFGLATV--KSRWSGSQQV	EQPTGSVLWMAPEV	516			
DB	381	IERMNYIHRDLRSANILVGNGLCKTADFLGARLIEDNEYTARQAK	FP---IKWTAPEA	437			
QY	517	IRMDQNNPFSQSDVSYGIVLYELMT-GELPYSHINNDDQIFWVG	RYASPOLSKLYK	575			
DB	438	ALY---GRTFIKSDWFSFGILLTELVTGRVFPYPGHNR-EVLEQ	VEGGERMP---CPQ	489			
QY	576	NCPRAMKRLVADCVKKKERPLFPQILSSIE	607				
DB	490	DCPTSLHELMTHCWKKDPEERTFEYIQSFLE	521				

Search completed: July 9, 2003, 09:52:20
Job time : 30 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2003, 09:44:12 ; Search time 18 Seconds
(without alignments)
1059.225 Million cell updates/sec

Title: US-09-637-302C-2

Perfect score: 3413

Sequence: 1 MEHIQGAWKTSINGFGPKDA.....AHTEDINACTLTSPRLPVF 648

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS-COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3413	100.0	648	1	US-08-276-151-2
2	3413	100.0	648	1	US-08-185-282-12
3	3413	100.0	648	2	US-08-886-751A-6
4	3413	100.0	648	3	US-09-209-668-13
5	3413	100.0	648	4	US-08-971-207-1
6	3331	97.6	648	1	US-08-185-282-3
7	3326	97.5	648	1	US-08-185-282-1
8	3325	97.4	648	1	US-08-185-282-2
9	3318	97.2	648	1	US-08-185-282-4
10	3299	96.7	648	1	US-08-185-282-5
11	1817	53.2	346	1	US-08-276-151-5
12	1641	48.1	315	1	US-08-571-758-12
13	1641	48.1	315	1	US-08-909-984A-12
14	1641	48.1	315	1	US-08-909-983-12
15	1373	40.2	257	1	US-08-077-256-1
16	1373	40.2	257	1	US-08-259-672-1
17	1373	40.2	257	1	US-08-459-351-1
18	1373	40.2	257	1	US-08-460-533-1
19	1373	40.2	257	5	PCT-US94-06654-1
20	1369	40.1	267	2	US-07-857-224B-42
21	1165	34.1	271	3	US-09-035-706-6
22	1165	34.1	271	3	US-08-955-841-6
23	1165	34.1	271	4	US-09-390-425-6
24	1165	34.1	271	4	US-09-566-906-6
25	1143	33.5	217	2	US-08-886-751A-5
26	1127.5	33.0	266	2	US-07-857-224B-43
27	1123	32.9	267	2	US-07-857-224B-45

28	1111.5	32.6	266	2	US-07-857-224B-44	Sequence 44, Appl
29	1071	31.4	197	1	US-08-276-151-3	Sequence 3, Appl1
30	1015	29.7	326	1	US-08-571-758-11	Sequence 11, Appl
31	1015	29.7	326	1	US-08-909-984A-11	Sequence 11, Appl
32	1015	29.7	326	1	US-08-909-983-11	Sequence 11, Appl
33	790	23.1	149	1	US-08-259-672-6	Sequence 6, Appl1
34	790	23.1	149	1	US-08-459-351-6	Sequence 6, Appl1
35	790	23.1	149	1	US-08-460-533-6	Sequence 6, Appl1
36	790	23.1	149	4	US-08-971-207-2	Sequence 2, Appl1
37	790	23.1	149	5	PCT-US94-06654-6	Sequence 2, Appl1
38	786	23.0	148	2	US-08-886-751A-4	Sequence 4, Appl1
39	753	22.1	147	1	US-08-276-151-4	Sequence 4, Appl1
40	575	16.8	966	1	US-08-571-758-2	Sequence 2, Appl1
41	575	16.8	966	1	US-08-909-984A-2	Sequence 2, Appl1
42	575	16.8	966	1	US-08-909-983-2	Sequence 2, Appl1
43	569.5	16.7	1003	1	US-08-571-758-4	Sequence 4, Appl1
44	569.5	16.7	1003	1	US-08-909-984A-4	Sequence 4, Appl1
45	569.5	16.7	1003	1	US-08-909-983-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-276-151-2
; Sequence 2, Application US/08276151
; Patent No. 5597719
; GENERAL INFORMATION:
; APPLICANT: Freed, Ellen
; APPLICANT: Ruggieri, Rosamaria
; TITLE OF INVENTION: Interaction of raf-1 and 14-3-3 Proteins
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward et al.
; STREET: Five Palo Alto Square
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,151
; FILING DATE: 14-JUL-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Ph.D., Timothy E
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: ONYX-005/0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5481
; TELEFAX: (415) 857-0663
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-151-2

Query Match 100.0%; Score 3413; DB 1; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.4e-293;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHIQGAWKTSINGFGKDAVFDGSSCISPTIVQQFGYQRRASDDGKLDPKSTNTIRV 60
Db 1 MEHIQGAWKTSINGFGKDAVFDGSSCISPTIVQQFGYQRRASDDGKLDPKSTNTIRV 60
QY 61 FLNPKRTVVVNRNGMSLHDLCKALKVRGLQPECCAVFRLHHEHGKARKLDWNTDAAS 120

Db 61 FLPNKQRTVNVNRNGSLHDCLMKALKVRLGQPECCAVFRLLEHHEGKKARLDWNTDAAS 120
QY 121 LIGELQVDFLDHVPVLTTHNFARKTFLKAFCDICQKFLNGRCOTCGYKPFHEHCSTKV 180
Db 121 LIGELQVDFLDHVPVLTTHNFARKTFLKAFCDICQKFLNGRCOTCGYKPFHEHCSTKV 180
QY 181 PTCVDSNTRQLLLFPNSIGSGVPALESLMRRMRESVSRMPVSSQHRSTPHAF 240
Db 181 PTCVDSNTRQLLLFPNSIGSGVPALESLMRRMRESVSRMPVSSQHRSTPHAF 240
QY 241 NTSSPSEGLSQRORSTSTPNVHMVSTTLVPSRMIEDAIRSHSESASPALSUSPNL 300
Db 241 NTSSPSEGLSQRORSTSTPNVHMVSTTLVPSRMIEDAIRSHSESASPALSUSPNL 300
QY 301 SPTGWSQPKTPVPAQRERAPVSGTQEKNIIRPGQRDSSYWEIEASEVYMLSTRIGSGSF 360
Db 301 SPTGWSQPKTPVPAQRERAPVSGTQEKNIIRPGQRDSSYWEIEASEVYMLSTRIGSGSF 360
QY 361 GTVYKGWHDGVAVKILKVVDPTPEQFOAFRNEVAVLRKTRHVNILLFVGYMTKDNLAI 420
Db 361 GTVYKGWHDGVAVKILKVVDPTPEQFOAFRNEVAVLRKTRHVNILLFVGYMTKDNLAI 420
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Db 421 TQWCEGSSLYKHLHVQETKFMQLDIARQTAQGM DY L HAKNI IHRDMKSNIFLHEGL 480
QY 481 TVKIGDFGLATVKSWSGSOQVEQPTGSLWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
Db 481 TVKIGDFGLATVKSWSGSOQVEQPTGSLWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
QY 541 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPRAMKRLVADCVKKYKEERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPRAMKRLVADCVKKYKEERPLFP 600
QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSRPLPVF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSRPLPVF 648

RESULT 2
US-08-185-282-12
; Sequence 12, Application US/08185282
; Patent No. 5618670
; GENERAL INFORMATION:
; APPLICANT: Rapp, Ulf R.
; APPLICANT: Storm, Stephen M.
; TITLE OF INVENTION: DETECTION METHOD FOR C-RAF-1 GENES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DAREY & CUSHMAN
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,282
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/759,738
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/82732
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000

TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-185-282-12
Query Match 100.0%; Score 3413; DB 1; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.4e-293;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHIOGAKWTISNGFGKDAVFDGSSCISPTIVQOFGYQRRASDDGKLTDPSTKNTIRV 60
Db 1 MEHIOGAKWTISNGFGKDAVFDGSSCISPTIVQOFGYQRRASDDGKLTDPSTKNTIRV 60
QY 61 FLPNKQRTVNVNRNGSLHDCLMKALKVRLGQPECCAVFRLLEHHEGKKARLDWNTDAAS 120
Db 61 FLPNKQRTVNVNRNGSLHDCLMKALKVRLGQPECCAVFRLLEHHEGKKARLDWNTDAAS 120
QY 121 LIGELQVDFLDHVPVLTTHNFARKTFLKAFCDICQKFLNGRCOTCGYKPFHEHCSTKV 180
Db 121 LIGELQVDFLDHVPVLTTHNFARKTFLKAFCDICQKFLNGRCOTCGYKPFHEHCSTKV 180
QY 181 PTCVDSNTRQLLLFPNSIGSGVPALESLMRRMRESVSRMPVSSQHRSTPHAF 240
Db 181 PTCVDSNTRQLLLFPNSIGSGVPALESLMRRMRESVSRMPVSSQHRSTPHAF 240
QY 241 NTSSPSEGLSQRORSTSTPNVHMVSTTLVPSRMIEDAIRSHSESASPALSUSPNL 300
Db 241 NTSSPSEGLSQRORSTSTPNVHMVSTTLVPSRMIEDAIRSHSESASPALSUSPNL 300
QY 301 SPTGWSQPKTPVPAQRERAPVSGTQEKNIIRPGQRDSSYWEIEASEVYMLSTRIGSGSF 360
Db 301 SPTGWSQPKTPVPAQRERAPVSGTQEKNIIRPGQRDSSYWEIEASEVYMLSTRIGSGSF 360
QY 361 GTVYKGWHDGVAVKILKVVDPTPEQFOAFRNEVAVLRKTRHVNILLFVGYMTKDNLAI 420
Db 361 GTVYKGWHDGVAVKILKVVDPTPEQFOAFRNEVAVLRKTRHVNILLFVGYMTKDNLAI 420
QY 421 TQWCEGSSLYKHLHVQETKFMQLDIARQTAQGM DY L HAKNI IHRDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKFMQLDIARQTAQGM DY L HAKNI IHRDMKSNIFLHEGL 480
QY 481 TVKIGDFGLATVKSWSGSOQVEQPTGSLWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
Db 481 TVKIGDFGLATVKSWSGSOQVEQPTGSLWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
QY 541 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPRAMKRLVADCVKKYKEERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPRAMKRLVADCVKKYKEERPLFP 600
QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSRPLPVF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSRPLPVF 648

RESULT 3
US-08-886-751A-6
; Sequence 6, Application US/08886751A
; Patent No. 5885783
; GENERAL INFORMATION:
; APPLICANT: Yoo, Tai-June
; APPLICANT: Cheng, Kuang-Chuan
; TITLE OF INVENTION: Autoimmune Inner Ear Disease Antigen and
; TITLE OF INVENTION: Diagnostic Assay
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta

STATE: Georgia
COUNTRY: U.S.A.
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886.751A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Young, Leona G.
REGISTRATION NUMBER: 37,266
REFERENCE/DOCKET NUMBER: 25490-0100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens

US-08-886-751A-6

Query Match 100.0%; Score 3413; DB 2; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.4e-293;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MEHIOGAWKTTISNGFGKDAVFDGSSCISPTIVQOFGYQRRASDDGKLTDPKTSNTIRV 60
QY 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFRLHHEHKGKARLDWNTDAAS 120
DB 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFRLHHEHKGKARLDWNTDAAS 120
QY 121 LIGELQVDFLDHVPVLTTHNFARKTFLKLAFCDCQKFLNGFCQTCGKFKHEHCSTKV 180
DB 121 LIGELQVDFLDHVPVLTTHNFARKTFLKLAFCDCQKFLNGFCQTCGKFKHEHCSTKV 180
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DB 181 PTMCDVMSNIROLLEFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRYSTPHAFTF 240
QY 241 NTSSPSSGSLSORQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSSPNNL 300
DB 241 NTSSPSSGSLSORQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSSPNNL 300
QY 301 SPTGWSQKTPVPAQREAPVSGTQENKIRPRGORDSSYYWEIEASEVMLSTRIGSGSF 360
DB 301 SPTGWSQKTPVPAQREAPVSGTQENKIRPRGORDSSYYWEIEASEVMLSTRIGSGSF 360
QY 361 GTVYKKGWHDVAVKILKVVDPTEQFAFRNEAVLRKTRHVNILLFMGYMTKDNLAIV 420
DB 361 GTVYKKGWHDVAVKILKVVDPTEQFAFRNEAVLRKTRHVNILLFMGYMTKDNLAIV 420
QY 421 TQWCEGSSLYKHLHVQETKQFQMLIDIAQTQAGMDYLHAKNIIHRDMKSNFIHLEGL 480
DB 421 TQWCEGSSLYKHLHVQETKQFQMLIDIAQTQAGMDYLHAKNIIHRDMKSNFIHLEGL 480
QY 481 TVKIGDFGLATVKSRWSSGQVEQPTGSLWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
DB 481 TVKIGDFGLATVKSRWSSGQVEQPTGSLWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540

QY 541 LMTGELPYSHINNRODQIIFWVGRYASPDLSKLYKNCPRAMKRLVADCKVKKEERPLFP 600
DB 541 LMTGELPYSHINNRODQIIFWVGRYASPDLSKLYKNCPRAMKRLVADCKVKKEERPLFP 600
QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRPFV 648
DB 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRPFV 648

RESULT 4

US-09-209-668-13
; Sequence 13, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; FILE REFERENCE: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
; FILE REFERENCE: ISPH-0336
; CURRENT APPLICATION NUMBER: US/09/209,668A
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-209-668-13

Query Match 100.0%; Score 3413; DB 3; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.4e-293;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHIOGAWKTTISNGFGKDAVFDGSSCISPTIVQOFGYQRRASDDGKLTDPKTSNTIRV 60
DB 1 MEHIOGAWKTTISNGFGKDAVFDGSSCISPTIVQOFGYQRRASDDGKLTDPKTSNTIRV 60
QY 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFRLHHEHKGKARLDWNTDAAS 120
DB 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFRLHHEHKGKARLDWNTDAAS 120
QY 121 LIGELQVDFLDHVPVLTTHNFARKTFLKLAFCDCQKFLNGFCQTCGKFKHEHCSTKV 180
DB 121 LIGELQVDFLDHVPVLTTHNFARKTFLKLAFCDCQKFLNGFCQTCGKFKHEHCSTKV 180
QY 181 PTMCDVMSNIROLLEFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRYSTPHAFTF 240
DB 181 PTMCDVMSNIROLLEFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRYSTPHAFTF 240
QY 241 NTSSPSSGSLSORQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSSPNNL 300
DB 241 NTSSPSSGSLSORQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSSPNNL 300
QY 301 SPTGWSQKTPVPAQREAPVSGTQENKIRPRGORDSSYYWEIEASEVMLSTRIGSGSF 360
DB 301 SPTGWSQKTPVPAQREAPVSGTQENKIRPRGORDSSYYWEIEASEVMLSTRIGSGSF 360
QY 361 GTVYKKGWHDVAVKILKVVDPTEQFAFRNEAVLRKTRHVNILLFMGYMTKDNLAIV 420
DB 361 GTVYKKGWHDVAVKILKVVDPTEQFAFRNEAVLRKTRHVNILLFMGYMTKDNLAIV 420
QY 421 TQWCEGSSLYKHLHVQETKQFQMLIDIAQTQAGMDYLHAKNIIHRDMKSNFIHLEGL 480
DB 421 TQWCEGSSLYKHLHVQETKQFQMLIDIAQTQAGMDYLHAKNIIHRDMKSNFIHLEGL 480
QY 481 TVKIGDFGLATVKSRWSSGQVEQPTGSLWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
DB 481 TVKIGDFGLATVKSRWSSGQVEQPTGSLWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
QY 541 LMTGELPYSHINNRODQIIFWVGRYASPDLSKLYKNCPRAMKRLVADCKVKKEERPLFP 600
DB 541 LMTGELPYSHINNRODQIIFWVGRYASPDLSKLYKNCPRAMKRLVADCKVKKEERPLFP 600

QY 601 QILSSIELQHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
Db 601 QILSSIELQHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 5
US-08-971-207-1
; Sequence 1, Application US/08971207
; Patent No. 6300081
; GENERAL INFORMATION:
; APPLICANT: Taylor, Stephen J.
; APPLICANT: Shalloway, David
; TITLE OF INVENTION: ACTIVATED RAS INTERACTION ASSAY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: P. O. Box 1051, Clinton Square
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION DATA:
; FILING DATE: US/08/971,207
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/030,924
; FILING DATE: 15-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-971-207-1

Query Match 100.0%; Score 3413; DB 4; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.4e-293;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHQGAWKTSINGFGKDAVFGDSSCISPTIVQFGYORRASDDGKLTDPKSTNTIRV 60
Db 1 MEHQGAWKTSINGFGKDAVFGDSSCISPTIVQFGYORRASDDGKLTDPKSTNTIRV 60
QY 61 FLNPKQRTVVVNRGMSLHDCMLKALKVRGLQPECCAVFRLHHEKKGKARLDWNTDAAS 120
Db 61 FLNPKQRTVVVNRGMSLHDCMLKALKVRGLQPECCAVFRLHHEKKGKARLDWNTDAAS 120
QY 121 LIGEELOVDPLDHVPLTTHNFARKTFLKAFCDICOKFLLNGFRCTCGYKKEHCSTKV 180
Db 121 LIGEELOVDPLDHVPLTTHNFARKTFLKAFCDICOKFLLNGFRCTCGYKKEHCSTKV 180
QY 181 PTMCDVMSNRQLLLFPNSTIGSGVPALPSLTMRMRRESVSRMPVSSQHRYSTPHAFF 240
Db 181 PTMCDVMSNRQLLLFPNSTIGSGVPALPSLTMRMRRESVSRMPVSSQHRYSTPHAFF 240
QY 241 NTSSPSSEGLSQRQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSPNL 300
Db 241 NTSSPSSEGLSQRQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSPNL 300

QY 301 SPTGWSQKTPVPAQRERAPVSGTOEKNKIRPGORDSSYYWEIEASEVMLSTRIGSGSF 360
Db 301 SPTGWSQKTPVPAQRERAPVSGTOEKNKIRPGORDSSYYWEIEASEVMLSTRIGSGSF 360
QY 361 GTVYKGWHDVAVKILKVVDPTEQFOAFNEVAVLRKTHVNLILFMGYMTKDNLAIV 420
Db 361 GTVYKGWHDVAVKILKVVDPTEQFOAFNEVAVLRKTHVNLILFMGYMTKDNLAIV 420
QY 421 TQWCEGSSLYKHLHVQETKFOFQOLIDIAROTAGQMDYLHAKNIIHRDMKSNNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKFOFQOLIDIAROTAGQMDYLHAKNIIHRDMKSNNIFLHEGL 480
QY 481 TVKIGDFGLATVYKRWGSGSQVEQPTGSLVMAPEVIRMODNNPFSQSDVSYGIVLYE 540
Db 481 TVKIGDFGLATVYKRWGSGSQVEQPTGSLVMAPEVIRMODNNPFSQSDVSYGIVLYE 540
QY 541 LMTGELPYSHINNRDQIIFMVGRGYASDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFMVGRGYASDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
QY 601 QILSSIELQHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
Db 601 QILSSIELQHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 6
US-08-185-282-3
; Sequence 3, Application US/08185282
; Patent No. 5618670
; GENERAL INFORMATION:
; APPLICANT: Rapp, Ulf R.
; APPLICANT: Storm, Stephen M.
; TITLE OF INVENTION: DETECTION METHOD FOR C-RAF-1 GENES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,282
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/759,738
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/3683/82732
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-185-282-3

Query Match 97.6%; Score 3331; DB 1; Length 648;
Best Local Similarity 97.5%; Pred. No. 2.5e-286;
Matches 632; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 1 MEHQGAWKTSINGFGKDAVFGDSSCISPTIVQFGYORRASDDGKLTDPKSTNTIRV 60

Db 1 MEHIQAWKTSINGFGLKDAVDFGSSCISPTIVQOFGYQRRASDDGKLTDSSTNTIRV 60
QY 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAAS 120
Db 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAAS 120
QY 121 LIGELQVDFLDHVPITTHNFARKTFLKAFCDICQKFLNGFRQTCGKFEHCSTKV 180
Db 121 LIGELQVDFLDHVPITTHNFARKTFLKAFCDICQKFLNGFRQTCGKFEHCSTKV 180
QY 181 PTMCVDSNIRQLLFPNSTIGDSGVPALSLTMRMRRESVSRMPVSSQHRYSSTPHAF 240
Db 181 PTMCVDSNIRQLLFPNSTIGDSGVPALSLTMRMRRESVSRMPVSSQHRYSSTPHAF 240
QY 241 NTSSPSSGSLSORQSTSTPNVHMVSTTLVDSRMIEDAIRSHSESASPSALSSSPNNL 300
Db 241 NTSSPSSGSLSORQSTSTPNVHMVSTTLVDSRMIEDAIRSHSESASPSALSSSPNNL 300
QY 301 SPTGWSQKTPVPAQERAPVSGTOEKNKIRPRGORDSSYYWEIEASEVMLSTRIGSGSF 360
Db 301 SPTGWSQKTPVPAQERAPVSGTOEKNKIRPRGORDSSYYWEIEASEVMLSTRIGSGSF 360
QY 361 GTVYKKGWHDVAVKILKVVDPTPEQOAFRNEVAVLRKTRHVNILLFMGYMTKDLAIV 420
Db 361 GTVYKKGWHDVAVKILKVVDPTPEQOAFRNEVAVLRKTRHVNILLFMGYMTKDLAIV 420
QY 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQOTAGMDYLHAKNIHHRDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQOTAGMDYLHAKNIHHRDMKSNIFLHEGL 480
QY 481 TVKIGDFGLATVKSRWGSQOQVEQPTGSLVLMWMAPEVIRMQDNNPFSQSDVYSYGI 540
Db 481 TVKIGDFGLATVKSRWGSQOQVEQPTGSLVLMWMAPEVIRMQDNNPFSQSDVYSYGI 540
QY 541 LMTGELPYSHINNRODQIIFWVGRYASPDLSKLYKNCPKAMKRLVADCVKKEERPLFP 600
Db 541 LMTGELPYSHINNRODQIIFWVGRYASPDLSKLYKNCPKAMKRLVADCVKKEERPLFP 600
QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 7

US-08-185-282-1
; Sequence 1, Application US/08185282
; Patent No. 5618670
; GENERAL INFORMATION:
; APPLICANT: Rapp, Ulf R.
; APPLICANT: Storm, Stephen M.
; TITLE OF INVENTION: DETECTION METHOD FOR C-RAF-1 GENES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,282
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/759,738
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/82732
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-185-282-1

Query Match 97.5%; Score 3326; DB 1; Length 648;
Best Local Similarity 97.4%; Pred. No. 6.9e-286;
Matches 631; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 MEHIQAWKTSINGFGLKDAVDFGSSCISPTIVQOFGYQRRASDDGKLTDSSTNTIRV 60
Db 1 MEHIQAWKTSINGFGLKDAVDFGSSCISPTIVQOFGYQRRASDDGKLTDSSTNTIRV 60
QY 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAAS 120
Db 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAAS 120
QY 121 LIGELQVDFLDHVPITTHNFARKTFLKAFCDICQKFLNGFRQTCGKFEHCSTKV 180
Db 121 LIGELQVDFLDHVPITTHNFARKTFLKAFCDICQKFLNGFRQTCGKFEHCSTKV 180
QY 181 PTMCVDSNIRQLLFPNSTIGDSGVPALSLTMRMRRESVSRMPVSSQHRYSSTPHAF 240
Db 181 PTMCVDSNIRQLLFPNSTIGDSGVPALSLTMRMRRESVSRMPVSSQHRYSSTPHAF 240
QY 241 NTSSPSSGSLSORQSTSTPNVHMVSTTLVDSRMIEDAIRSHSESASPSALSSSPNNL 300
Db 241 NTSSPSSGSLSORQSTSTPNVHMVSTTLVDSRMIEDAIRSHSESASPSALSSSPNNL 300
QY 301 SPTGWSQKTPVPAQERAPVSGTOEKNKIRPRGORDSSYYWEIEASEVMLSTRIGSGSF 360
Db 301 SPTGWSQKTPVPAQERAPVSGTOEKNKIRPRGORDSSYYWEIEASEVMLSTRIGSGSF 360
QY 361 GTVYKKGWHDVAVKILKVVDPTPEQOAFRNEVAVLRKTRHVNILLFMGYMTKDLAIV 420
Db 361 GTVYKKGWHDVAVKILKVVDPTPEQOAFRNEVAVLRKTRHVNILLFMGYMTKDLAIV 420
QY 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQOTAGMDYLHAKNIHHRDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQOTAGMDYLHAKNIHHRDMKSNIFLHEGL 480
QY 481 TVKIGDFGLATVKSRWGSQOQVEQPTGSLVLMWMAPEVIRMQDNNPFSQSDVYSYGI 540
Db 481 TVKIGDFGLATVKSRWGSQOQVEQPTGSLVLMWMAPEVIRMQDNNPFSQSDVYSYGI 540
QY 541 LMTGELPYSHINNRODQIIFWVGRYASPDLSKLYKNCPKAMKRLVADCVKKEERPLFP 600
Db 541 LMTGELPYSHINNRODQIIFWVGRYASPDLSKLYKNCPKAMKRLVADCVKKEERPLFP 600
QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 8

US-08-185-282-2
; Sequence 2, Application US/08185282
; Patent No. 5618670
; GENERAL INFORMATION:
; APPLICANT: Rapp, Ulf R.
; APPLICANT: Storm, Stephen M.
; TITLE OF INVENTION: DETECTION METHOD FOR C-RAF-1 GENES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

Db 241 NTSSPSSEGLSQRSTSTPNVHMVSTTLRVDSRMIEDAIRSHSESASPSALSSPNNL 300
Qy 301 SPTGWSQPKTPVPAQRERAPVSGTQEKNIKIRPGORDSSYYWEIEASEVLMSTRIGSGF 360
Db 301 SPTGWSQPKTPVPAQRERAPVSGTQEKNIKIRPGORDSSYYWEIEASEVLMSTRIGSGF 360
Qy 361 GTVYKGHWGDAVKILKVVDPPTPEQQAQFNEVAVLRKTRHVNILLFMCYMTKDNLAIV 420
Db 361 GTVYKGHWGDAVKILKVVDPPTPEQQAQFNEVAVLRKTRHVNILLFMCYMTKDNLAIV 420
Qy 421 TOWCEGSSLYKHLHVQETKFMQLIDIAQOTAGMDYLHAKNIIHRDMKSNIFLHEGL 480
Db 421 TOWCEGSSLYKHLHVQETKFMQLIDIAQOTAGMDYLHAKNIIHRDMKSNIFLHEGL 480
Qy 481 TVKIGDFGLATVKSRSWGSQVQEQPTGSLWMAPEVIRMQDNNPFSQSDVYSGIVLYE 540
Db 481 TVKIGDFGLATVKSRSWGSQVQEQPTGSLWMAPEVIRMQDNNPFSQSDVYSGIVLYE 540
Qy 541 LMTGELPYSHINNRDQIIFVWGRGYASPDLSKLYKNCPCAMKRLVADCVKVKKEERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFVWGRGYASPDLSKLYKNCPCAMKRLVADCVKVKKEERPLFP 600
Qy 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVPF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVPF 648

RESULT 10

US-08-185-282-5
; Sequence 5, Application US/08185282
; Patent No. 5618670
; GENERAL INFORMATION:
; APPLICANT: Rapp, Ulf R.
; APPLICANT: Storm, Stephen M.
; TITLE OF INVENTION: DETECTION METHOD FOR C-RAF-1 GENES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DAREY & CUSHMAN
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,282
; FILING DATE:
; CLASSIFICATION: 435

; PRIOR APPLICATION NUMBER: US/07/159,738
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/82732
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-185-282-5

Query Match 96.7%; Score 3299; DB 1; Length 648;
Best Local Similarity 96.8%; Pred. No. 1.7e-283;

Matches 627; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
Qy 1 MEHIQGAWKTIISNGFGFKDAVDFGSSCISPTIVQFGYORRASDDGKLTDPKSTNTIRV 60
Db 1 MEHIQGAWKTIISNGFGFKDAVDFGSSCISPTIVQFGYORRASDDGKLTDPKSTNTIRV 60
Qy 61 FLPNKQRTVYVNRNGMSLHDCLMKALKVRGLQPECCAVFRLHHEHKGKARLDWNTDAAS 120
Db 61 FLPNKQRTVYVNRNGMSLHDCLMKALKVRGLQPECCAVFRLHHEHKGKARLDWNTDAAS 120
Qy 121 LIGEELOVDFLHVPLTTHNFARKTFLKLAFCIDICOKFLNFRQOTCGYKPEHCSTKV 180
Db 121 LIGEELOVDFLHVPLTTHNFARKTFLKLAFCIDICOKFLNFRQOTCGYKPEHCSTKV 180
Qy 181 PTMCDVWSNIRQLLLFPNSTIGDSGVPALPSITMRMRRESVSRMPVSSOHRYSTPHATTF 240
Db 181 PTMCDVWSNIRQLLLFPNSTIGDSGVPALPSITMRMRRESVSRMPVSSOHRYSTPHATTF 240
Qy 241 NTSSPSSEGLSQRQSTSTPNVHMVSTTLRVDSRMIEDAIRSHSESASPSALSSPNNL 300
Db 241 NTSSPSSEGLSQRQSTSTPNVHMVSTTLRVDSRMIEDAIRSHSESASPSALSSPNNL 300
Qy 301 SPTGWSQPKTPVPAQRERAPVSGTQEKNIKIRPGORDSSYYWEIEASEVLMSTRIGSGF 360
Db 301 SPTGWSQPKTPVPAQRERAPVSGTQEKNIKIRPGORDSSYYWEIEASEVLMSTRIGSGF 360
Qy 361 GTVYKGHWGDAVKILKVVDPPTPEQQAQFNEVAVLRKTRHVNILLFMCYMTKDNLAIV 420
Db 361 GTVYKGHWGDAVKILKVVDPPTPEQQAQFNEVAVLRKTRHVNILLFMCYMTKDNLAIV 420
Qy 421 TOWCEGSSLYKHLHVQETKFMQLIDIAQOTAGMDYLHAKNIIHRDMKSNIFLHEGL 480
Db 421 TOWCEGSSLYKHLHVQETKFMQLIDIAQOTAGMDYLHAKNIIHRDMKSNIFLHEGL 480
Qy 481 TVKIGDFGLATVKSRSWGSQVQEQPTGSLWMAPEVIRMQDNNPFSQSDVYSGIVLYE 540
Db 481 TVKIGDFGLATVKSRSWGSQVQEQPTGSLWMAPEVIRMQDNNPFSQSDVYSGIVLYE 540
Qy 541 LMTGELPYSHINNRDQIIFVWGRGYASPDLSKLYKNCPCAMKRLVADCVKVKKEERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFVWGRGYASPDLSKLYKNCPCAMKRLVADCVKVKKEERPLFP 600
Qy 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVPF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVPF 648

RESULT 11

US-08-276-151-5
; Sequence 5, Application US/08276151
; Patent No. 5597719
; GENERAL INFORMATION:
; APPLICANT: Freed, Ellen
; APPLICANT: Ruggieri, Rosamaria
; TITLE OF INVENTION: Interaction of raf-1 and 14-3-3 Proteins
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward et al.
; STREET: Five Palo Alto Square
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,151
; FILING DATE: 14-JUL-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Torchia, Ph.D., Timothy E
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: ONYX-005/000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5481
; TELEFAX: (415) 857-0663
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-276-151-5

Query Match
Best Local Similarity 53.28; Score 1817; DB 1; Length 346;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 TGWSQKTPVPAQRERAPVSGTQEKNNKIRPRGORDSSYYWEIEASEVYMLSTRIGSGSFGT 362
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 TGWSQKTPVPAQRERAPVSGTQEKNNKIRPRGORDSSYYWEIEASEVYMLSTRIGSGSFGT 60

QY 363 VYKGKWHGDVAVKILKVVDPTPEQFQAFRNEVAVLAKTRHVNILLFMGYMTKDNLAIVTQ 422
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 VYKGKWHGDVAVKILKVVDPTPEQFQAFRNEVAVLAKTRHVNILLFMGYMTKDNLAIVTQ 120

QY 423 MCEGSSLYKHLHVQETKTFQFQIDIDARQTAQGM DYLHAKNIIHRDMKSNINFLHEGLTV 482
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 MCEGSSLYKHLHVQETKTFQFQIDIDARQTAQGM DYLHAKNIIHRDMKSNINFLHEGLTV 180

QY 483 KIGDFGLATVKRSWGSQQVEQPTGVSVMWAPVIRMQDNNPFSTQSDYSYGVLYELM 542
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 KIGDFGLATVKRSWGSQQVEQPTGVSVMWAPVIRMQDNNPFSTQSDYSYGVLYELM 240

QY 543 TCELPYSHINNRDQIIFWVGRYASPDLSKLYKNCPKAMKRLVADCCVKVKRERPLFPQI 602
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 241 TCELPYSHINNRDQIIFWVGRYASPDLSKLYKNCPKAMKRLVADCCVKVKRERPLFPQI 300

QY 603 LSSIELLQHSLPKINRSASPSLHRAAHTEDINACTLTTSPLRPVF 648
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 301 LSSIELLQHSLPKINRSASPSLHRAAHTEDINACTLTTSPLRPVF 346

```

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; APPLICATION NUMBER: US/08/571,758
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B96-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
;
US-08-571-758-12

Query Match 48.1%; Score 1641; DB 1; Length 315;
Best Local Similarity 99.7%; Pred. No. 3.5e-137;
Matches 314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 334 GORDSSVYWEIEASEVMLSFRIGSGSGTYYKKGWGDVAVKILKVVDPTPEQFOAPRNE 393
Db 1 GORDSSVYWEIEASEVMLSFRIGSGSGTYYKKGWGDVAVKILKVVDPTPEQFOAPRNE 60

QY 394 VAVLRKTRHYNILLFMCYMTKDNLAIYVTCWCEGSSLYKKHLHVQETKQFQLIDIAKQTA 453
Db 61 VAVLRKTRHYNILLFMCYMTKDNLAIYVTCWCEGSSLYKKHLHVQETKQFQLIDIAKQTA 120

QY 454 QGMDYLHAKNIIHRDMKSNIFLEHGTVTKIGDFGLATVKSRSWGSQOVQPTGCVLWMA 513
Db 121 QGMDYLHAKNIIHRDMKSNIFLEHGTVTKIGDFGLATVKSRSWGSQOVQPTGCVLWMA 180

QY 514 PEVIRMDNNPFSQSDVYISYGIYLYELMTGELPYSHINNRDQIFVMVGRGIASPDLSKL 573
Db 181 PEVIRMDNNPFSQSDVYISYGIYLYELMTGELPYSHINNRDQIFVMVGRGIASPDLSKL 240

QY 574 YKNCPPAKMKRLVADVCKVKKEERPLFPQILSSITELLOHSLPKINRSASEPSLHRAATED 633
Db 241 YKNCPPAKMKRLVADVCKVKKEERPLFPQILSSITELLOHSLPKINRSASEPSLHRAATED 300

QY 634 INACTLTSPRLPVF 648
Db 301 INACTLTSPRLPVF 315

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RESOLUTION 12
US-08-571-758-12
; Sequence 12, Application US/08571758
; Patent No. 5700675
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerry M.
; APPLICANT: Therrien, Marc
; APPLICANT: Chang, Henry C.
; APPLICANT: Karim, Felix D.
; APPLICANT: Wasserman, David A.
; TITLE OF INVENTION: A No. 5700675el Protein Kinase Required for Ras
; TITLE OF INVENTION: Signal Transduction
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

RESULT 13
US-08-909-984A-12
Sequence 12, Application US/08909984A
Patent No. 5747275
GENERAL INFORMATION:
APPLICANT: Rubin, Gerry M.
APPLICANT: Therrien, Marc
APPLICANT: Chang, Henry C.
APPLICANT: Karim, Felix D.
APPLICANT: Massarman, David A.
TITLE OF INVENTION: A No. 5747275el Protein Kinase Required for Ras
TITLE OF INVENTION: Signal transduction
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/909,984A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B96-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
;
US-08-909-984A-12

Query Match 48.1%; Score 1641; DB 1; Length 315;
Best Local Similarity 99.7%; Pred. No. 3.5e-137;
Matches 314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 334 GORDSSYYWEIEASEVMLSTRIGSGFGTVYKKGWGDVAVKILKVVDPTPEQFAFRNE 393
Db 1 GORDSSYYWEIEASEVMLSTRIGSGFGTVYKKGWGDVAVKILKVVDPTPEQFAFRNE 60

Qy 394 VAVLRKTRHVNILLFMGYMTKDNLAIVTQWCEGSSLYKHLHVQETKFMQFLIDIAQRTA 453
Db 61 VAVLRKTRHVNILLFMGYMTKDNLAIVTQWCEGSSLYKHLHVQETKFMQFLIDIAQRTA 120

Qy 454 QGMDYLHAKNIIHRDKSNINFLHEGLTVKIGDFGLATVKSRSWGSGQVEQPTGSLVWMA 513
Db 121 QGMDYLHAKNIIHRDKSNINFLHEGLTVKIGDFGLATVKSRSWGSGQVEQPTGSLVWMA 180

Qy 514 PEVIRMODNPPFSQSDVSYGIVLYELMTGELPYSHINNRDQIIFMVGRGYASPDLSKL 573
Db 181 PEVIRMODNPPFSQSDVSYGIVLYELMTGELPYSHINNRDQIIFMVGRGYASPDLSKL 240

Qy 574 YKNCPRAMKRLVADCVKVKKEERPLFPQILSSIELLQHSPLKINRSASEPSLHRAAHTED 633
Db 634 INACTLTTSPLRPVF 648
301 INACTLTTSPLRPVF 315

RESULT 14
US-08-909-983-12
; Sequence 12, Application US/08909983
; Patent No. 5747288
;
GENERAL INFORMATION:
; APPLICANT: Rubin, Gerry M.
; APPLICANT: Therrien, Marc
; APPLICANT: Chang, Henry C.
; APPLICANT: Karim, Felix D.
; APPLICANT: Wasserman, David A.
; TITLE OF INVENTION: A No. 5747288el Protein Kinase Required for Ras
; TITLE OF INVENTION: Signal transduction
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/909,983
; FILING DATE: 12-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/571,758
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B96-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
;
US-08-909-983-12

Query Match 48.1%; Score 1641; DB 1; Length 315;
Best Local Similarity 99.7%; Pred. No. 3.5e-137;
Matches 314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 334 GORDSSYYWEIEASEVMLSTRIGSGFGTVYKKGWGDVAVKILKVVDPTPEQFAFRNE 393
Db 1 GORDSSYYWEIEASEVMLSTRIGSGFGTVYKKGWGDVAVKILKVVDPTPEQFAFRNE 60

Qy 394 VAVLRKTRHVNILLFMGYMTKDNLAIVTQWCEGSSLYKHLHVQETKFMQFLIDIAQRTA 453
Db 61 VAVLRKTRHVNILLFMGYMTKDNLAIVTQWCEGSSLYKHLHVQETKFMQFLIDIAQRTA 120

Qy 454 QGMDYLHAKNIIHRDKSNINFLHEGLTVKIGDFGLATVKSRSWGSGQVEQPTGSLVWMA 513
Db 121 QGMDYLHAKNIIHRDKSNINFLHEGLTVKIGDFGLATVKSRSWGSGQVEQPTGSLVWMA 180

Qy 514 PEVIRMODNPPFSQSDVSYGIVLYELMTGELPYSHINNRDQIIFMVGRGYASPDLSKL 573
Db 181 PEVIRMODNPPFSQSDVSYGIVLYELMTGELPYSHINNRDQIIFMVGRGYASPDLSKL 240

Qy 574 YKNCPRAMKRLVADCVKVKKEERPLFPQILSSIELLQHSPLKINRSASEPSLHRAAHTED 633
Db 241 YKNCPRAMKRLVADCVKVKKEERPLFPQILSSIELLQHSPLKINRSASEPSLHRAAHTED 300

634 INACTLTTSPLRPVF 648
301 INACTLTTSPLRPVF 315

RESULT 15
US-08-077-256-1
; Sequence 1, Application US/08077256
; Patent No. 5582995
;
GENERAL INFORMATION:
; APPLICANT: Joseph Avruch, M.D.
; APPLICANT: Xian-feng Zhang, Ph.D.
; TITLE OF INVENTION: INHIBITING PROTEIN
; TITLE OF INVENTION: INTERACTIONS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
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OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,256
FILING DATE: 19930611
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark, Esq.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/190001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 257
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
us-08-077-256-1

Query Match 40.2%; Score 1373; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.4e-113;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	FLPNKQRTVVNVNMGSLHDCLMKALKVRGLQPECCAVFLLHEHKGKARLDWNTDAAS	120
Db	61	FLPNKQRTVVNVNMGSLHDCLMKALKVRGLQPECCAVFLLHEHKGKARLDWNTDAAS	120
QY	121	LIGEEQVDFLDHVPLTTHNFARKTFLKAFCDICQKFLNGFRCTCGYKFHEHCSTKV	180
Db	121	LIGEEQVDFLDHVPLTTHNFARKTFLKAFCDICQKFLNGFRCTCGYKFHEHCSTKV	180
QY	181	PTMCVDWSNIROQLLPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSOHRYSTPHFTF	240
Db	181	PTMCVDWSNIROQLLPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSOHRYSTPHFTF	240
QY	241	NTSSPSSEGSLSQRQRS	257
Db	241	NTSSPSSEGSLSQRQRS	257

Search completed: July 9, 2003, 09:47:06
Job time : 21 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2003, 09:35:32 ; Search time 41 seconds
(without alignments)
2106.010 Million cell updates/sec

Title: US-09-637-302c-2

Perfect score: 3413

Sequence: 1 MEHIQAWKTIISNGFGKDA.....AHTEDINACTLTSPRLPVF 648

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3413	100.0	648	17	AA198215 Human Raf1 kinase.
2	3413	100.0	648	18	AA17044 Human c-raf 1 prot
3	3413	100.0	648	18	AA17044 Human Raf-1. Homo
4	3413	100.0	648	19	AA17044 Human Raf-1. Homo
5	3413	100.0	648	20	AA17044 Homo sapiens GST-R
6	3413	100.0	648	20	AA17044 Human c-raf-1 prot
7	3413	100.0	648	21	AA17044 Human ORF2465
8	3413	100.0	648	21	AA17044 Amino acid sequenc
9	3413	100.0	648	21	AA17044 Human c-raf protei
10	3413	100.0	648	22	AA170295 Human c-Raf protei

11	3413	100.0	648	22	AA17044 Amino acid sequenc
12	3413	100.0	648	22	AA17044 Amino acid sequenc
13	3413	100.0	648	23	AA17044 Human protein kina
14	3413	100.0	648	23	AA17044 Human c-raf-1 prot
15	3413	100.0	648	23	AA17044 Raf-1 fusion pr
16	3413	100.0	648	23	AA17044 Raf-1 fusion pr
17	3413	100.0	648	23	AA17044 Human c-raf-1. Ho
18	3413	100.0	648	23	AA17044 Human c-raf-1 prot
19	3413	100.0	648	23	AA17044 Mutant mouse c-raf
20	3413	100.0	648	23	AA17044 Mutant mouse c-raf
21	3413	100.0	648	23	AA17044 Mouse c-raf-1. Mu
22	3413	100.0	648	23	AA17044 Mouse c-raf-1 prot
23	3413	100.0	648	23	AA17044 Mutant mouse c-raf
24	3413	100.0	648	23	AA17044 Mutant mouse c-raf
25	3413	100.0	648	23	AA17044 Mutant mouse c-raf
26	3413	100.0	648	23	AA17044 Mutant mouse c-raf
27	3413	100.0	648	23	AA17044 Mutant mouse c-raf
28	3413	100.0	648	23	AA17044 Mouse mutant c-raf
29	3413	100.0	648	23	AA17044 Mouse mutant c-raf
30	3413	100.0	648	23	AA17044 Mouse mutant c-raf
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32	3413	100.0	648	23	AA17044 Mouse mutant c-raf
33	3413	100.0	648	23	AA17044 Mouse mutant c-raf
34	3413	100.0	648	23	AA17044 Human v-raf protei
35	3413	100.0	648	23	AA17044 Human protein kina
36	3413	100.0	648	23	AA17044 Human B-raf protei
37	3413	100.0	648	23	AA17044 Drosophila melanog
38	3413	100.0	648	23	AA17044 Raf(1-257) oncopro
39	3413	100.0	648	23	AA17044 Ras-binding fragme
40	3413	100.0	648	23	AA17044 Ras-binding fragme
41	3413	100.0	648	23	AA17044 Yeast protein kina
42	3413	100.0	648	23	AA17044 Sequence encoded b
43	3413	100.0	648	23	AA17044 T18 oncogene prod.
44	3413	100.0	648	23	AA17044 Homo sapiens GSR-R
45	3413	100.0	648	23	AA17044 Amino acid sequenc

ALIGNMENTS

RESULT 1
ID AAR98215 standard; Protein; 648 AA.
XX AAR98215;
AC AAR98215;
XX 24-SEP-1996 (first entry)
DT Human Raf1 kinase.
DE CDC25; phosphatase; Raf protein; proliferative disorder; cancer;
KW leukemia; psoriasis; bone disorder; fibroproliferative disorders;
KW differentiation associated disorder; kinase; chronic neurodegenerative disease; vascular disorder.
XX Homo sapiens.
OS WO9612820-A1.
XX 02-MAY-1996.
PD 23-OCT-1995; 95WO-US13661.
PF 24-OCT-1994; 94US-0328239.
PR (COLD-) COLD SPRING HARBOR LAB.
PA Beach DH, Galaktionov K, Jessus C;
PI WPI; 1996-230619/23.
DR N-PSDB; AAT30085.
XX Identification of cpds. which modulate and inhibit ras-mediated

PT activation of CDC25 - useful in treatment of proliferative disorders
PT and differentiation associated disorders, e.g. chronic
PT neurodegenerative diseases

XX Claim 14; Page 44-47; 52pp; English.

CC CDC25 phosphatases (e.g. AAT30082-T30084) and Raf proteins (e.g.
CC AAT30085) are able to physically interact to form protein-protein
CC complexes, with the Raf protein mediating the activation of CDC25
CC phosphatases. Modulators and inhibitors of ras-mediated CDC25
CC activation and modulators and inhibitors of interaction between
CC CDC25 phosphatase and Raf-kinase can be used in the treatment
CC of proliferative disorders, e.g. cancers, leukemias, psoriasis,
CC bone disorders, fibroproliferative disorders, differentiation
CC associated disorders, e.g. chronic neurodegenerative diseases,
CC vascular disorders and disorders associated with degenerative
CC changes in glandular cells and the inhibition of spermatogenesis.

XX SQ Sequence 648 AA;

Query Match 100.0%; Score 3413; DB 17; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.1e-298;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHIQAWKTTISNGFGKDAVDFGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60
DB 1 MEHIQAWKTTISNGFGKDAVDFGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60
QY 61 FLNPKQRTVVVNRNGSLHDCLMKALKVRLGLOPECCAVFRLLEHKGKARLDWNTDAAS 120
DB 61 FLNPKQRTVVVNRNGSLHDCLMKALKVRLGLOPECCAVFRLLEHKGKARLDWNTDAAS 120
QY 121 LIGEEQVDFLDHVPVLTTHNFARKTEFLKAFCDICQKFLNGFRQCOTCGYKFEHCSTKV 180
DB 121 LIGEEQVDFLDHVPVLTTHNFARKTEFLKAFCDICQKFLNGFRQCOTCGYKFEHCSTKV 180
QY 181 PTMCDVMSNRQLLLFPNSTIGDGVGVPALPSLTMRMRRESVSRMPVSSQHRYSSTPHAFTE 240
DB 181 PTMCDVMSNRQLLLFPNSTIGDGVGVPALPSLTMRMRRESVSRMPVSSQHRYSSTPHAFTE 240
QY 241 NTSSPSSGSLSQORSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPALSPPNNL 300
DB 241 NTSSPSSGSLSQORSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPALSPPNNL 300
QY 301 SPTGWSQPKTPVPAQERAPVSGTQEKNIKIRPRGDRSSYYWEIEASEVMLSTRIGSGSF 360
DB 301 SPTGWSQPKTPVPAQERAPVSGTQEKNIKIRPRGDRSSYYWEIEASEVMLSTRIGSGSF 360
QY 361 GTVYKKGWHDVAVKILKVVDPTPEQFAFRNEVAVLRKTRHVNILLFMGYTKDLNLAIV 420
DB 361 GTVYKKGWHDVAVKILKVVDPTPEQFAFRNEVAVLRKTRHVNILLFMGYTKDLNLAIV 420
QY 421 TOMCEGSSLYKHLHVQETKQFQMLIDIAQTAQGMIDYLAHAKNIHRDKSNIFLHEGL 480
DB 421 TOMCEGSSLYKHLHVQETKQFQMLIDIAQTAQGMIDYLAHAKNIHRDKSNIFLHEGL 480
QY 481 TVKIGDFGLATVSRSGSQVQEPQGVSLWMAPEVIRMQDNNPFSQSDVYSYGLVLYE 540
DB 481 TVKIGDFGLATVSRSGSQVQEPQGVSLWMAPEVIRMQDNNPFSQSDVYSYGLVLYE 540
QY 541 LMTGELPYSHINNRDQIIFWVGRYASPDLSKLYKNCPRAMKRLVADCVKKYKEERPLFP 600
DB 541 LMTGELPYSHINNRDQIIFWVGRYASPDLSKLYKNCPRAMKRLVADCVKKYKEERPLFP 600
QY 601 QILSSIELLQHSILPKINRSASEPSLHRAAHTEDINACTLTTSPLPVF 648
DB 601 QILSSIELLQHSILPKINRSASEPSLHRAAHTEDINACTLTTSPLPVF 648

RESULT 2

AAW17044

ID AAW17044 standard; Protein: 648 AA.

XX

AC AAW17044;
XX 07-JUL-1997 (first entry)
XX Human c-raf 1 protein used in diagnosis of lymphoma or lung cancer.
DE
XX
XX raf; oncogene; lymphoma; lung cancer; neoplasia; point mutation;
KW conserved region; adenocarcinoma; codon 533; diagnosis; detection.
XX
OS Homo sapiens.
XX US5618670-A.
PN 08-APR-1997.
PD 26-AUG-1988; 88US-0236947.
PF 16-SEP-1991; 91US-0759738.
PR 26-AUG-1988; 88US-0236947.
PR 24-JAN-1994; 94US-0185282.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Rapp DR, Storm SM;
PI WPI; 1997-225421/20.
DR N-PSDB; AAT68800.
XX
PT Classification of lymphoma or lung cancer - on the basis of a point
PT mutation in c-raf-1 gene
XX
PS Claim 2; Column 35-38; 26pp; English.
XX
CC AAW17044, the human c-raf-1 protein, was used in a method for
CC classifying a lymphoma or lung cancer in an individual. The method
CC involves detecting the presence of a point mutation in a conserved region
CC of the c-raf-1 gene (codon 533, encoding Ser, in this sequence) derived
CC from lymphoma or lung cancer tissue and classifying the lymphoma or lung
CC cancer as a c-raf-1 mutation-associated cancer if one or more point
CC mutations are present. The method is particularly applicable to lung
CC adenocarcinoma.
XX
SQ Sequence 648 AA;

Query Match 100.0%; Score 3413; DB 18; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.1e-298;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHIQAWKTTISNGFGKDAVDFGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60
DB 1 MEHIQAWKTTISNGFGKDAVDFGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60
QY 61 FLNPKQRTVVVNRNGSLHDCLMKALKVRLGLOPECCAVFRLLEHKGKARLDWNTDAAS 120
DB 61 FLNPKQRTVVVNRNGSLHDCLMKALKVRLGLOPECCAVFRLLEHKGKARLDWNTDAAS 120
QY 121 LIGEEQVDFLDHVPVLTTHNFARKTEFLKAFCDICQKFLNGFRQCOTCGYKFEHCSTKV 180
DB 121 LIGEEQVDFLDHVPVLTTHNFARKTEFLKAFCDICQKFLNGFRQCOTCGYKFEHCSTKV 180
QY 181 PTMCDVMSNRQLLLFPNSTIGDGVGVPALPSLTMRMRRESVSRMPVSSQHRYSSTPHAFTE 240
DB 181 PTMCDVMSNRQLLLFPNSTIGDGVGVPALPSLTMRMRRESVSRMPVSSQHRYSSTPHAFTE 240
QY 241 NTSSPSSGSLSQORSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPALSPPNNL 300
DB 241 NTSSPSSGSLSQORSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPALSPPNNL 300
QY 301 SPTGWSQPKTPVPAQERAPVSGTQEKNIKIRPRGDRSSYYWEIEASEVMLSTRIGSGSF 360
DB 301 SPTGWSQPKTPVPAQERAPVSGTQEKNIKIRPRGDRSSYYWEIEASEVMLSTRIGSGSF 360
QY 361 GTVYKKGWHDVAVKILKVVDPTPEQFAFRNEVAVLRKTRHVNILLFMGYTKDLNLAIV 420

Db 361 GTVYKRGHGDVAVKILVVDPTPEQFAFRNEVAVLRKTRHVNILLFMGTWTKDNLAI 420
QY 421 TQWCEGSSLYKHLHVOETKFOFQOLIDTAROTAGMDYLHAKNIHRDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVOETKFOFQOLIDTAROTAGMDYLHAKNIHRDMKSNIFLHEGL 480
QY 481 TVKIGDFGLATVKSRWSGQVEQPTGSLVWMAPEVIRMDONNPFQSDVYSYGVLYE 540
Db 481 TVKIGDFGLATVKSRWSGQVEQPTGSLVWMAPEVIRMDONNPFQSDVYSYGVLYE 540
QY 541 LMTGELPYSHINNRDQIIFMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKERPLFP 600
QY 601 QILSSIellohSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVE 648
Db 601 QILSSIellohSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVE 648
RESULT 3
AAW13107
ID AAW13107 standard; Protein; 648 AA.
AC AAW13107;
XX
DT 12-MAY-1997 (first entry)
DE Human Raf-1.
KW Human; raf-1; complex; 14-3-3; beta; zeta; modulation; binding;
KW detection; screening; interaction; cell cycle; control; neoplasia;
KW pathological condition; drug.
XX
OS Homo sapiens.
FH Key
FT Region
FT 1..197 Location/Qualifiers
FT /note= "conserved region 1 containing region"
FT 186..332
FT /note= "conserved region 2 containing region"
XX
PN US5597719-A.
XX
XX 28-JAN-1997.
XX
XX 14-JUL-1994; 94US-0276151.
XX
XX 14-JUL-1994; 94US-0276151.
XX (ONYX-) ONYX PHARM INC.
XX
PI Freed E, Ruggieri R;
XX
XX WPI; 1997-108327/10.
DR N-PSDB; AAT61894.
XX
PT Complex of raf-1 and 14-3-3 polypeptide(s) - useful for anticancer
PT drug screening
XX
XX Disclosure; Columns 31-38; 43pp; English.
PS
CC The present sequence is human Raf-1, which can be used in a
CC novel composition comprising a complex of human Raf-1, or a
CC fragment comprising residues 1-197 or 186-332, or lacking residues
CC 51-131, and a 14-3-3 polypeptide (preferably human 14-3-3 beta or
CC zeta). The composition can be used to screen for drugs which
CC modulate the binding interaction between Raf-1 and 14-3-3,
CC especially to identify drugs that modulate Raf-1 mediated cell
CC cycle control, and/or neoplastic or other pathological conditions
CC dependent on the interaction between Raf-1 and 14-3-3 beta or zeta.
XX
XX Sequence 648 AA;

Query Match 100.0%; Score 3413; DB 18; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.1e-298;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHIQGAWKTSINGFGFKDAVFDGSGSCISPTIVQFGYQRRASDDGKLTDPKSTNTIRV 60
Db 1 MEHIQGAWKTSINGFGFKDAVFDGSGSCISPTIVQFGYQRRASDDGKLTDPKSTNTIRV 60
QY 61 FLNPKQRTVYVNRNGMSLHDLKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAAS 120
Db 61 FLNPKQRTVYVNRNGMSLHDLKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAAS 120
QY 121 LIGBELQVDFLDHVPILTTNFAKTFELKLAFCDICOKFLNGFRCTCGVKFHERGSTRV 180
Db 121 LIGBELQVDFLDHVPILTTNFAKTFELKLAFCDICOKFLNGFRCTCGVKFHERGSTRV 180
QY 181 PTMCVMSNTRQQLLLFPNSTIGDGVPAIPSLPMRRMRRESVSRMPVSSQHRYSTPHATTF 240
Db 181 PTMCVMSNTRQQLLLFPNSTIGDGVPAIPSLPMRRMRRESVSRMPVSSQHRYSTPHATTF 240
QY 241 NTSSPSEGSLSORQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSPNNL 300
Db 241 NTSSPSEGSLSORQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSPNNL 300
QY 301 SPTGWSQKTPVPAQREAPVSGTQEKNIIRPGQDSSYIWEIEASEVYMLSTRIGSGSF 360
Db 301 SPTGWSQKTPVPAQREAPVSGTQEKNIIRPGQDSSYIWEIEASEVYMLSTRIGSGSF 360
QY 361 GTVYKRGHGDVAVKILVVDPTPEQFAFRNEVAVLRKTRHVNILLFMGTWTKDNLAI 420
Db 361 GTVYKRGHGDVAVKILVVDPTPEQFAFRNEVAVLRKTRHVNILLFMGTWTKDNLAI 420
QY 421 TQWCEGSSLYKHLHVOETKFOFQOLIDTAROTAGMDYLHAKNIHRDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVOETKFOFQOLIDTAROTAGMDYLHAKNIHRDMKSNIFLHEGL 480
QY 481 TVKIGDFGLATVKSRWSGQVEQPTGSLVWMAPEVIRMDONNPFQSDVYSYGVLYE 540
Db 481 TVKIGDFGLATVKSRWSGQVEQPTGSLVWMAPEVIRMDONNPFQSDVYSYGVLYE 540
QY 541 LMTGELPYSHINNRDQIIFMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKERPLFP 600
QY 601 QILSSIellohSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVE 648
Db 601 QILSSIellohSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVE 648
RESULT 4
AAW62220
ID AAW62220 standard; protein; 648 AA.
XX
XX AAW62220;
AC AAW62220;
XX
XX 17-SEP-1998 (first entry)
DT
DE Raf-1 protein.
XX
KW ras binding domain; raf-1; ras interaction assay; detection; diagnosis;
KW activated; oncogene; malignant; human; cancer; leukaemia.
XX
OS Homo sapiens.
XX WO9821585-A1.
PN
XX 22-MAY-1998.
PD
XX 14-NOV-1997; 97WO-US21351.
PF
XX 15-NOV-1996; 96US-0030924.
PR
XX

PA (CORR) CORNELL RES FOUND INC.
XX Shalloway D, Taylor SJ;
XX WPI; 1998-298109/26.
XX Detecting activated ras protein from capture by immobilised protein
PT - having ras-binding domain, used for diagnosis and prognosis of
PT cancers involving mutated ras genes
XX
XX Disclosure; Page 10-12; 47pp; English.
XX
XX A method has been developed for detecting activated ras protein (I).
XX The method comprises: (i) immobilising a protein (II) containing a
XX ras-binding domain on a support; (ii) incubating (II) with
XX (I)-containing lysate from cultured cells, and (iii) determining
XX amount of (I) bound to (II). The present sequence represents a
XX raf-1 protein from the present invention. The method is used for
XX diagnosis and prognosis of malignancies (e.g. cancer of breast, colon,
XX lung or pancreas, also some forms of leukemia) related to (I) in
XX humans, i.e. where a mutation in a ras gene causes constitutive
XX activation. It may also be used to study normal regulation of (I) and
XX to evaluate compounds for activation of (I) in cultured cells. The
XX method: (i) does not require pretreatment of samples with radioisotopes,
XX so can be used to measure activation levels in whole tissue samples;
XX (ii) can detect specifically any of the individual ras isoforms, or all
XX forms collectively, and (iii) can detect all potential activating
XX mutations or activation in response to activation of other oncogenes.
XX
SQ Sequence 648 AA;

Query Match 100.0%; Score 3413; DB 19; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.1e-298;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEHIQAWKTSINGFGFKDAVDFGSSCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60
Db 1 MEHIQAWKTSINGFGFKDAVDFGSSCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60
Qy 61 FLPNKQRTVVVNRNGMSLHDCMLKALKVRLGLOPECCAVFLLHKGKARLDWNTDAAS 120
Db 61 FLPNKQRTVVVNRNGMSLHDCMLKALKVRLGLOPECCAVFLLHKGKARLDWNTDAAS 120
Qy 121 LIGELQVDFLDHVPLTTHNFARKFLKAFCDICQKFLNGFCQTCGYFHEHCSTKV 180
Db 121 LIGELQVDFLDHVPLTTHNFARKFLKAFCDICQKFLNGFCQTCGYFHEHCSTKV 180
Qy 181 PTMCVDSNIRQLLLFPNSTIGDGVPPALPSLTMRMRRESVSRMPVSSQHRYSTPHAFTF 240
Db 181 PTMCVDSNIRQLLLFPNSTIGDGVPPALPSLTMRMRRESVSRMPVSSQHRYSTPHAFTF 240
Qy 241 NTSSPSSEGLSQRSQSTSTPNVHMVSTTLTPVDSRMIEDAIRSHSESASPSALSSPNNL 300
Db 241 NTSSPSSEGLSQRSQSTSTPNVHMVSTTLTPVDSRMIEDAIRSHSESASPSALSSPNNL 300
Qy 301 SPTGWSOPKTPVAQRAERAPVSGTOBKNIIRPRGORDSSVYWEIASEVWLSPRIGSGSF 360
Db 301 SPTGWSOPKTPVAQRAERAPVSGTOBKNIIRPRGORDSSVYWEIASEVWLSPRIGSGSF 360
Qy 361 GTVYKGWHDGVAVKILKVVDPTPEQFQAFRNEVAVLKRTRHVNILLFMGYMTKDLAIV 420
Db 361 GTVYKGWHDGVAVKILKVVDPTPEQFQAFRNEVAVLKRTRHVNILLFMGYMTKDLAIV 420
Qy 421 TOWCEGSSLYKHLVQETKQFQMDIARQTAQGMIDYLAHAKNIIRDMKSNIFLHEGL 480
Db 421 TOWCEGSSLYKHLVQETKQFQMDIARQTAQGMIDYLAHAKNIIRDMKSNIFLHEGL 480
Qy 481 TVKIGDGLATVSRWSSGQVQPTGSLVWMAPEVIRMDNNPFQSDVTSYGLVLYE 540
Db 481 TVKIGDGLATVSRWSSGQVQPTGSLVWMAPEVIRMDNNPFQSDVTSYGLVLYE 540
Qy 541 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600

Db 541 LMTGELPYSHINNRDQIIFVMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
Qy 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRPVF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLRPVF 648

RESULT 5
AAW95611
ID AAW95611 standard; peptide; 648 AA.
XX
XX AAW95611;
AC
XX 08-JUN-1999 (first entry)
DT
XX Homo sapiens GST-Raf-1 protein.
DE
XX Homo sapiens GST-Raf-1 protein.
KW Inner ear; 28kD antigen; Meniere's disease; membranous structure;
KW autoimmune disease; immunotherapy; Raf-1 protein.
XX
XX Homo sapiens.
OS
XX WO9901085-A2.
PN
XX 14-JAN-1999.
PD
XX
XX 01-JUL-1998; 98WO-US13796.
PF
XX
XX 02-JUL-1997; 97US-0886751.
PR
XX
XX (CHEN/) CHENG K.
PA (YOOT/) YOO T.
XX
XX Cheng K, Yoo T;
PI
XX
XX WPI; 1999-105735/09.
DR
XX
XX A new antigen of the inner ear membranous structure - useful to
PT diagnose Meniere's disease
XX
XX Disclosure; Page 26-30; 38pp; English.
PS
XX
XX The sequence is that of a Raf-1 N-terminal fragment which was used
CC in the production of a 28kD antigen from the membranous structure
CC of the inner ear (MIE antigen), reactive with antibodies from
CC patients having Meniere's disease. It can be used as part of a
CC method of detecting Meniere's disease in an animal or human and
CC to distinguish Meniere's disease from other autoimmune inner ear
CC diseases, to monitor the disease progression and effects of
CC treatment, and to provide an antigen for immunotherapeutic
CC treatment of the disease.
XX
SQ Sequence 648 AA;

Query Match 100.0%; Score 3413; DB 20; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.1e-298;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEHIQAWKTSINGFGFKDAVDFGSSCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60
Db 1 MEHIQAWKTSINGFGFKDAVDFGSSCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60
Qy 61 FLPNKQRTVVVNRNGMSLHDCMLKALKVRLGLOPECCAVFLLHKGKARLDWNTDAAS 120
Db 61 FLPNKQRTVVVNRNGMSLHDCMLKALKVRLGLOPECCAVFLLHKGKARLDWNTDAAS 120
Qy 121 LIGELQVDFLDHVPLTTHNFARKFLKAFCDICQKFLNGFCQTCGYFHEHCSTKV 180
Db 121 LIGELQVDFLDHVPLTTHNFARKFLKAFCDICQKFLNGFCQTCGYFHEHCSTKV 180
Qy 181 PTMCVDSNIRQLLLFPNSTIGDGVPPALPSLTMRMRRESVSRMPVSSQHRYSTPHAFTF 240
Db 181 PTMCVDSNIRQLLLFPNSTIGDGVPPALPSLTMRMRRESVSRMPVSSQHRYSTPHAFTF 240

QY 241 NTSSPSEGLSQRQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSPNNL 300
DB 241 NTSSPSEGLSQRQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSPNNL 300
QY 301 SPTGNSQPTPVPQAQERAPVSGTQEKNIIRPRGQSDSYWEIEASEVMLSTRIGSGSF 360
DB 301 SPTGNSQPTPVPQAQERAPVSGTQEKNIIRPRGQSDSYWEIEASEVMLSTRIGSGSF 360
QY 361 GTVYKKGWGDVAVKTLKVVDPTEQFQAFRNEVAVLRKTRHVNILLFMGYMTKDNLAIV 420
DB 361 GTVYKKGWGDVAVKTLKVVDPTEQFQAFRNEVAVLRKTRHVNILLFMGYMTKDNLAIV 420
QY 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQTAQGMVYLHAKNIIHRDMKSNIFLHEGL 480
DB 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQTAQGMVYLHAKNIIHRDMKSNIFLHEGL 480
QY 481 TVKIGDFGLATVKSRSWGSQOQVEPTGSLVMAPEVIRMQDNNPFSQSDVYSYGIYLYE 540
DB 481 TVKIGDFGLATVKSRSWGSQOQVEPTGSLVMAPEVIRMQDNNPFSQSDVYSYGIYLYE 540
QY 541 LMTGELPYSHINNNDQIIFWVGSGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
DB 541 LMTGELPYSHINNNDQIIFWVGSGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
DB 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 6

AAW30664
ID AAW30664 standard; Protein; 648 AA.

XX AAW30664;

AC AAW30664;

XX AAW30664;

DT 08-APR-1999 (first entry)

XX Human c-raf-1 protein.

DE Human; c-raf-1; oncogene; cancer; lung adenocarcinoma.

XX Homo sapiens.

OS US5869308-A.

XX 09-FEB-1999.

XX 01-APR-1997; 97US-0831317.

XX 16-SEP-1991; 91US-0759738.

XX 26-AUG-1988; 88US-0236947.

XX 24-JAN-1994; 94US-0185282.

XX 01-APR-1997; 97US-0831317.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Rapp UR, Storm SM;

XX WPI; 1999-152776/13.

XX N-PSDB; AAX03925.

XX New isolated human nucleic acid unique to c-raf-1 - having a point mutation in the conserved region encoding amino acids 450-630 of a 648 amino acid sequence

XX Claim 1; Column 35-38; 26pp; English.

XX The present sequence represents human c-raf-1. The present invention describes c-raf-1 having a point mutation in the conserved region encoding amino acids 450-630 (preferably amino acid 533) of the human c-raf-1 protein. Point mutations in the conserved region (CR3 - the kinase domain) of c-raf-1 protein is indicative of increased risk of

CC developing cancer (particularly lung adenocarcinoma) and determining the appropriate course of treatment.

XX Sequence 648 AA;

Query Match 100.0%; Score 3413; DB 20; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.le-298;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHQCAWKTISNGFGKDAVDFDSSCISPTIVQOFGYQRRASDGLTDPSTKTSNIRV 60
DB 1 MEHQCAWKTISNGFGKDAVDFDSSCISPTIVQOFGYQRRASDGLTDPSTKTSNIRV 60

QY 61 FLPNKQRTVNVNRNGMSLHDCMLKALKVGRLOPCCAVFRLHHEHKKKARLDNNTDAAS 120
DB 61 FLPNKQRTVNVNRNGMSLHDCMLKALKVGRLOPCCAVFRLHHEHKKKARLDNNTDAAS 120

QY 121 LIGBELOVDFLDHVPFLTHNFARKTFLKAFCDICQKFLNGFRQCOTCGYKFHEHCSTKV 180
DB 121 LIGBELOVDFLDHVPFLTHNFARKTFLKAFCDICQKFLNGFRQCOTCGYKFHEHCSTKV 180

QY 181 PTMCVDRSNIRQLLFPNSTIGDGVLPALPSLTHRRMRESVSRMPVSOHRYSTPHAFTE 240
DB 181 PTMCVDRSNIRQLLFPNSTIGDGVLPALPSLTHRRMRESVSRMPVSOHRYSTPHAFTE 240

QY 241 NTSSPSEGLSQRQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSPNNL 300
DB 241 NTSSPSEGLSQRQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSPNNL 300

QY 301 SPTGNSQPTPVPQAQERAPVSGTQEKNIIRPRGQSDSYWEIEASEVMLSTRIGSGSF 360
DB 301 SPTGNSQPTPVPQAQERAPVSGTQEKNIIRPRGQSDSYWEIEASEVMLSTRIGSGSF 360

QY 361 GTVYKKGWGDVAVKTLKVVDPTEQFQAFRNEVAVLRKTRHVNILLFMGYMTKDNLAIV 420
DB 361 GTVYKKGWGDVAVKTLKVVDPTEQFQAFRNEVAVLRKTRHVNILLFMGYMTKDNLAIV 420

QY 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQTAQGMVYLHAKNIIHRDMKSNIFLHEGL 480
DB 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQTAQGMVYLHAKNIIHRDMKSNIFLHEGL 480

QY 481 TVKIGDFGLATVKSRSWGSQOQVEPTGSLVMAPEVIRMQDNNPFSQSDVYSYGIYLYE 540
DB 481 TVKIGDFGLATVKSRSWGSQOQVEPTGSLVMAPEVIRMQDNNPFSQSDVYSYGIYLYE 540

QY 541 LMTGELPYSHINNNDQIIFWVGSGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
DB 541 LMTGELPYSHINNNDQIIFWVGSGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600

QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
DB 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 7

AAW42701
ID AAW42701 standard; Protein; 648 AA.

XX AAW42701;

AC AAW42701;

XX AAW42701;

DT 08-FEB-2001 (first entry)

XX Human ORF2465 polypeptide sequence SEQ ID NO:4930.

Human; open reading frame; ORF; detection; cytostatic; hepatotropic; vulnerable; antiproliferative; antiparkinsonian; neurotropic; neuroprotective; anticonvulsant; osteopathic; antithrombotic; immunosuppressant; cardiac; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antihypertensive; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;

KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive.
XX Homo sapiens.
XX WO200058473-A2.
PN 05-OCT-2000.
PD 31-MAR-2000; 2000WO-US08621.
XX 31-MAR-1999; 99US-0127607.
PR 02-APR-1999; 99US-0127636.
PR 05-APR-1999; 99US-0127728.
PR 30-MAR-2000; 2000US-0540763.
XX (CURA-) CURAGEN CORP.
PA Shinkets RA, Leach M;
PI WPI; 2000-602362/57.
DR N-PSDB; AAC76910.
XX Novel nucleic acids and peptides derived from open reading frame x,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
XX Claim 11; Page 4106-4107; 5507pp; English.
XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
CC antiparasitic; antiparkinsonian; neurotropic; neuroprotective;
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatologic; immunosuppressive;
CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC antihypertensive; and antianemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORFX-associated disorder. The
CC nucleic acids can be used to express ORFX proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX Sequence 648 AA;
SQ Query Match 100.0%; Score 3413; DB 21; Length 648;
Best Local Similarity 100.0%; Pred. NO.1.le-298;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHTQGAWKTSNGFGKDAVDFGSSCISPTIVQFGYQRRASDQGLTDPKSTNTIRV 60
DB 1 MEHTQGAWKTSNGFGKDAVDFGSSCISPTIVQFGYQRRASDQGLTDPKSTNTIRV 60
QY 61 FLPNKQRTVVNRNGMSLHDCMLKALKVRLQGLQPECCAVFRLLEHKGKKARLDWNTDAAS 120
DB 61 FLPNKQRTVVNRNGMSLHDCMLKALKVRLQGLQPECCAVFRLLEHKGKKARLDWNTDAAS 120
QY 121 LIGELQVDFLDHVPPLTHNFARTFLKAFCDICQKFLNGRCQTCGKYKFFHEHGSTKV 180
DB 121 LIGELQVDFLDHVPPLTHNFARTFLKAFCDICQKFLNGRCQTCGKYKFFHEHGSTKV 180
QY 181 PTMCVDWSNIRQLLLFPNSTIGDSGVPALPSLTMRRRESVSRMPVSSQHRYSTPHAFTF 240

DB 181 PTMCVDWSNIRQLLLFPNSTIGDSGVPALPSLTMRRRESVSRMPVSSQHRYSTPHAFTF 240
QY 241 NTSSPSSGSLSQORQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPALSSPNL 300
DB 241 NTSSPSSGSLSQORQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPALSSPNL 300
QY 301 SPTGWSQKTPVPAQRERAPVSGTQEKNNKIRPGQDSSYYWEIDASEVMLSTRIGSGSF 360
DB 301 SPTGWSQKTPVPAQRERAPVSGTQEKNNKIRPGQDSSYYWEIDASEVMLSTRIGSGSF 360
QY 361 GTVYKKGWGDVAVKILKVVDDPTPQFAFRNEVAVLKRTHVNILLFPGYTKDNLAIV 420
DB 361 GTVYKKGWGDVAVKILKVVDDPTPQFAFRNEVAVLKRTHVNILLFPGYTKDNLAIV 420
QY 421 TQWCEGSSLYKHLHVQETKFMQFOLIDTARQTAQGMIDLHAKNIHHRDKNNIFLHEGL 480
DB 421 TQWCEGSSLYKHLHVQETKFMQFOLIDTARQTAQGMIDLHAKNIHHRDKNNIFLHEGL 480
QY 481 TVKIGDFGLATVKSRWSGQQVEQPTGSLVMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
DB 481 TVKIGDFGLATVKSRWSGQQVEQPTGSLVMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
QY 541 LMTGELPYSHINRDQILFMVGRGYASPDLSKLYKNCPRAMKRLVADCKVKKEERPLFP 600
DB 541 LMTGELPYSHINRDQILFMVGRGYASPDLSKLYKNCPRAMKRLVADCKVKKEERPLFP 600
QY 601 QILSSIELLQHSPLKINRSASEPSLHRAAHTEDINACTLTTSPLPVF 648
DB 601 QILSSIELLQHSPLKINRSASEPSLHRAAHTEDINACTLTTSPLPVF 648
RESULT 8
AAB08773
ID AAB08773 standard; protein; 648 AA.
XX AAB08773;
AC AAB08773;
XX 02-JAN-2001 (first entry)
XX Amino acid sequence of a human Raf-1 protein.
DE Intracellular signal transduction protein; antigen;
KW Systemic Lupus Erythematosus; inner ear; Raf-1.
XX Homo sapiens.
OS WO200050455-A2.
XX 31-AUG-2000.
XX 25-FEB-2000; 2000WO-US04770.
XX 25-FEB-1999; 99US-0121547.
XX (TALI/) TAI J Y.
XX Yoo TJ;
XX WPI; 2000-572070/53.
DR New 28 kDa antigen of the intracellular signal transduction protein,
PT useful for Systemic Lupus Erythematosus diagnosis, monitoring and
PT treatment -
XX Example 4; Page 17-19; 36pp; English.
XX The present sequence represents a human Raf-1 protein. The Raf-1
CC protein is homologous to an antigen of the intracellular signal
CC transduction protein. The antigen is reactive with antibodies from
CC patients with Systemic Lupus Erythematosus. The 28 kDa antigen is
CC present in the membranous fraction of the inner ear. The 28 kDa
CC antigen is useful for detecting Systemic Lupus Erythematosus in

CC animals, especially humans. The antigen is also useful for
 CC immunotherapeutic treatment of Systemic Lupus Erythematosus.

XX
 SQ Sequence 648 AA;

Query Match 100.0%; Score 3413; DB 21; Length 648;
 Best Local Similarity 100.0%; Pred. No. 1.1e-298;
 Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHIQAWKTSINGFGKDAVDFGSSCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60
 DB 1 MEHIQAWKTSINGFGKDAVDFGSSCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60

QY 61 FLPNKQRTVYVNRNGMSLHDCMLKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAAS 120
 DB 61 FLPNKQRTVYVNRNGMSLHDCMLKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAAS 120

QY 121 LIGEEQLQVDFLDHVPLTTHNFARKTFLKAFCDICQKFLNGFRCTCGYKFHEHCSTKV 180
 DB 121 LIGEEQLQVDFLDHVPLTTHNFARKTFLKAFCDICQKFLNGFRCTCGYKFHEHCSTKV 180

QY 181 PTMCVDWSNIRQLLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHYRSTPHATF 240
 DB 181 PTMCVDWSNIRQLLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHYRSTPHATF 240

QY 241 NTSSPSSEGSLSQRORSTSTPNVHMVSTLTPVDSRMIEDAIRSHSESASPSALSSPNL 300
 DB 241 NTSSPSSEGSLSQRORSTSTPNVHMVSTLTPVDSRMIEDAIRSHSESASPSALSSPNL 300

QY 301 SPTGWSQKTPVPAQERAPVSGTQEKNIKIRPGORDSSYWEIEASEVMLSTRIGSGSF 360
 DB 301 SPTGWSQKTPVPAQERAPVSGTQEKNIKIRPGORDSSYWEIEASEVMLSTRIGSGSF 360

QY 361 GTVYKKGWGDVAVKILKVVDPTPEQFAFRNEAVLRKTRHVNILLFMGYMTKDNLAIV 420
 DB 361 GTVYKKGWGDVAVKILKVVDPTPEQFAFRNEAVLRKTRHVNILLFMGYMTKDNLAIV 420

QY 421 TQWCGSSLYKHLHQETKQFQOLIDARTQAQMDYLHAKNIHHRDKMKNITFLHREGL 480
 DB 421 TQWCGSSLYKHLHQETKQFQOLIDARTQAQMDYLHAKNIHHRDKMKNITFLHREGL 480

QY 481 TVKIGDFGLATVKSWSGQVEQPTGSLVMAPEVIRMQDNNPFSQDVSYGIVLYE 540
 DB 481 TVKIGDFGLATVKSWSGQVEQPTGSLVMAPEVIRMQDNNPFSQDVSYGIVLYE 540

QY 541 LMTGELPYSHINRQIIIFMVGRYASPDLSKLYKNCPKAMRLVADCVKVKERPLFP 600
 DB 541 LMTGELPYSHINRQIIIFMVGRYASPDLSKLYKNCPKAMRLVADCVKVKERPLFP 600

QY 601 QILSSIELLOHSLPKINRSASPSLHRAAHTEDINACTLTTSPLPVPF 648
 DB 601 QILSSIELLOHSLPKINRSASPSLHRAAHTEDINACTLTTSPLPVPF 648

RESULT 9
 AAY94501

XX AAY94501 standard; Protein; 648 AA.

AC AAY94501;

XX 20-SEP-2000 (first entry)

XX Human c-ras protein.

KW Antisense; E-selectin; TNF alpha; cell adhesion; human;
 KW tumour necrosis factor alpha; phosphorothioate; methoxyethoxy;
 KW sepsis; rheumatoid arthritis; inflammatory; immune disease;
 KW inflammatory bowel disease; allergic contact dermatitis; psoriasis;
 KW diabetes; Grave's disease; allograft rejection; cancer; antibacterial;
 KW immunosuppressive; antipsoriatic; antidiabetic; antithyroid;
 KW cytostatic; dermatological; antiallergic; Ha-ras; c-ras;
 KW c-Jun N-terminal kinase; JNK; ds.

XX

OS Homo sapiens.
 XX WO200034303-A1.

XX 15-JUN-2000.

XX 08-DEC-1999; 99WO-US28965.

XX 10-DEC-1998; 98US-0209668.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Xu XS;

XX WPI; 2000-423367/36.

XX N-PSDB; AAA48654.

XX Modulating cell adhesion molecule expression for treating immune or
 XX inflammatory diseases involves treating cell with specific inhibitor of
 XX Tumour Necrosis Factor alpha signalling molecule

XX Disclosure; Page 83-85; 100pp; English.

XX A novel method for modulating cell adhesion molecule expression
 CC involves antisense inhibition of a tumour necrosis factor (TNF) alpha
 CC signalling molecule. In the method TNF alpha signalling molecules
 CC Ha-ras, c-ras and c-Jun N-terminal kinase (JNK)2 were inhibited by
 CC antisense oligonucleotides. In addition an antisense oligonucleotide
 CC to the cell adhesion molecule E-selectin was also examined. The
 CC present sequence is human c-ras protein. The DNA encoding this sequence
 CC was used to generate the c-ras antisense oligonucleotide. The antisense
 CC oligonucleotides used in the method contained modifications,
 CC namely phosphorothioate linkages and 2'methoxyethoxy bases. Some
 CC C residues also had a 5'methyl modification. Inhibitors of the TNF
 CC alpha signalling molecules have antibacterial, immunosuppressive,
 CC antipsoriatic, antidiabetic, antithyroid, cytostatic, dermatological,
 CC antiinflammatory and antiinflammatory activity. The antisense inhibitors
 CC may be useful for the treatment of sepsis, rheumatoid arthritis,
 CC inflammatory, immune disease, inflammatory bowel disease, allergic
 CC contact dermatitis, psoriasis, diabetes, Grave's disease, allograft
 CC rejection and cancer.

XX Sequence 648 AA;

Query Match 100.0%; Score 3413; DB 21; Length 648;
 Best Local Similarity 100.0%; Pred. No. 1.1e-298;
 Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHIQAWKTSINGFGKDAVDFGSSCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60
 DB 1 MEHIQAWKTSINGFGKDAVDFGSSCISPTIVQOFGYQRRASDDGKLTDPKSTNTIRV 60

QY 61 FLPNKQRTVYVNRNGMSLHDCMLKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAAS 120
 DB 61 FLPNKQRTVYVNRNGMSLHDCMLKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAAS 120

QY 121 LIGEEQLQVDFLDHVPLTTHNFARKTFLKAFCDICQKFLNGFRCTCGYKFHEHCSTKV 180
 DB 121 LIGEEQLQVDFLDHVPLTTHNFARKTFLKAFCDICQKFLNGFRCTCGYKFHEHCSTKV 180

QY 181 PTMCVDWSNIRQLLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHYRSTPHATF 240
 DB 181 PTMCVDWSNIRQLLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHYRSTPHATF 240

QY 241 NTSSPSSEGSLSQRORSTSTPNVHMVSTLTPVDSRMIEDAIRSHSESASPSALSSPNL 300
 DB 241 NTSSPSSEGSLSQRORSTSTPNVHMVSTLTPVDSRMIEDAIRSHSESASPSALSSPNL 300

QY 301 SPTGWSQKTPVPAQERAPVSGTQEKNIKIRPGORDSSYWEIEASEVMLSTRIGSGSF 360
 DB 301 SPTGWSQKTPVPAQERAPVSGTQEKNIKIRPGORDSSYWEIEASEVMLSTRIGSGSF 360

QY 361 GTVYKKGWGDVAVKILKVVDPTPEQFAFRNEAVLRKTRHVNILLFMGYMTKDNLAIV 420

Db 361 GTVYKGWHDVAVKILKVVDPTEQFAFRNEVAVLRKTRHVNILLFYGIMTKDLAIY 420
Qy 421 TQWCEGSSLYKHLHVQETKFMQLDIARQTAQGM DYLHAKNIHRDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKFMQLDIARQTAQGM DYLHAKNIHRDMKSNIFLHEGL 480
Qy 481 TVKIGDFGLATVKSWSGSGQVQPTGSLVWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
Db 481 TVKIGDFGLATVKSWSGSGQVQPTGSLVWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
Qy 541 LMTGELPYSHINNRDQIIFWVGSGYASPDLSKLYKNCPRAMKRLVADCVKVKKEERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFWVGSGYASPDLSKLYKNCPRAMKRLVADCVKVKKEERPLFP 600
Qy 601 QILSSIELLQHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVPF 648
Db 601 QILSSIELLQHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVPF 648
RESULT 10
AAB70295
ID AAB70295 standard; Protein; 648 AA.
XX AAB70295;
DT 10-MAY-2001 (first entry)
DE Human c-Raf protein.
KW Raf; ras; vector; tumour; arthritis; retinopathy; angioplasty.
XX Homo sapiens.
PN WO200112210-A1.
PD 22-FEB-2001.
PF 11-AUG-2000; 2000WO-US21842.
PR 13-AUG-1999; 99US-0148924.
PR 05-JUL-2000; 2000US-0215951.
PA (SCRI) SCRIPPS RES INST.
XX Hood J, Elliceiri B, Cheresh DA;
PI WPI; 2001-202826/20.
DR Composition for modulating angiogenesis and treating rheumatoid
PT arthritis and restenosis comprises Raf protein or viral or non-viral
PT gene transfer vector containing nucleic acid encoding for Raf or Ras
PT protein -
XX Disclosure; Fig 8; 102pp; English.
XX The present invention relates to a composition with a
CC Raf protein or a viral or non-viral gene transfer vector containing
CC a nucleic acid encoding for a Raf or Ras protein. The Raf
CC protein optionally has kinase activity and the Ras protein has
CC angiogenesis modulating activity. The invention is useful for
CC modulating angiogenesis in a tissue which has poor or abnormal
CC circulation, in a tissue which is a solid tumor or solid tumour
CC metastasis, in an inflamed tissue associated with arthritis or
CC rheumatoid arthritis, in a retinal tissue associated with retinopathy,
CC diabetic retinopathy or macular degeneration, or in a tissue which is
CC at the site of coronary angioplasty associated with restenosis.
XX Sequence 648 AA;
SQ Query Match 100.0%; Score 3413; DB 22; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.1e-298;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEHIQAWKTTISNGFGFKDAVDFDSSCISPTIVQOFGYQRRASDDGKLTDPKTSNTIRV 60
Db 1 MEHIQAWKTTISNGFGFKDAVDFDSSCISPTIVQOFGYQRRASDDGKLTDPKTSNTIRV 60
Qy 61 FLPNKQRTVVNVRNGMSLHDCIMKALKVKGLOPECCAVFRLLEHKGKARLDWNTDAAS 120
Db 61 FLPNKQRTVVNVRNGMSLHDCIMKALKVKGLOPECCAVFRLLEHKGKARLDWNTDAAS 120
Qy 121 LIGELQVDFLDHVPPLTTHNFARKTFKLAFCDICQKFLNGFRQCQCGYKFHCHCSTKV 180
Db 121 LIGELQVDFLDHVPPLTTHNFARKTFKLAFCDICQKFLNGFRQCQCGYKFHCHCSTKV 180
Qy 181 PTMCVDMNSNIQQLLFPNSTIGDGVPPALPSLTWRRMRESVSRMPVSSQHRYSPTPHAF 240
Db 181 PTMCVDMNSNIQQLLFPNSTIGDGVPPALPSLTWRRMRESVSRMPVSSQHRYSPTPHAF 240
Qy 241 NTSSPSSSEGLSQORSTSTPNVHMVSTLPLVDSPMIEDAIRSHESASPSALSSPNNL 300
Db 241 NTSSPSSSEGLSQORSTSTPNVHMVSTLPLVDSPMIEDAIRSHESASPSALSSPNNL 300
Qy 301 SPTGWSQPKTPVPAQRERAPVSGTQEKNKIRPRQORDSSYYWEIEASEVMLSTRIGSGSF 360
Db 301 SPTGWSQPKTPVPAQRERAPVSGTQEKNKIRPRQORDSSYYWEIEASEVMLSTRIGSGSF 360
Qy 361 GTVYKGWHDVAVKILKVVDPTEQFAFRNEVAVLRKTRHVNILLFYGIMTKDLAIY 420
Db 361 GTVYKGWHDVAVKILKVVDPTEQFAFRNEVAVLRKTRHVNILLFYGIMTKDLAIY 420
Qy 421 TQWCEGSSLYKHLHVQETKFMQLDIARQTAQGM DYLHAKNIHRDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKFMQLDIARQTAQGM DYLHAKNIHRDMKSNIFLHEGL 480
Qy 481 TVKIGDFGLATVKSWSGSGQVQPTGSLVWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
Db 481 TVKIGDFGLATVKSWSGSGQVQPTGSLVWMAPEVIRMQDNNPFSQSDVSYGIVLYE 540
Qy 541 LMTGELPYSHINNRDQIIFWVGSGYASPDLSKLYKNCPRAMKRLVADCVKVKKEERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFWVGSGYASPDLSKLYKNCPRAMKRLVADCVKVKKEERPLFP 600
Qy 601 QILSSIELLQHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVPF 648
Db 601 QILSSIELLQHSLPKINRSASEPSLHRAAHTEDINACTLTTSPLPVPF 648
RESULT 11
AAG67440
ID AAG67440 standard; Protein; 648 AA.
XX AAG67440;
AC AAG67440;
DT 26-NOV-2001 (first entry)
DE Amino acid sequence of a human polypeptide.
XX Human; protein kinase; protein phosphatase; signal transduction;
KW intracellular signalling pathway.
XX Homo sapiens.
PN WO200109345-A1.
XX 08-FEB-2001.
PD 28-JUL-2000; 2000WO-JP05060.
PR 29-JUL-1999; 99JP-0248036.
PR 18-OCT-1999; 99US-0159590.
PR 11-JAN-2000; 2000JP-0118776.
PR 17-FEB-2000; 2000US-0183322.
PR 02-MAY-2000; 2000JP-0183767.
XX

(HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
 PI Senoo C, Nezu J;

DR WPI: 2001-564736/63.

XX New genes encoding protein kinase and protein phosphatase, useful for
 PT identifying modulators which can be used to treat human or animal
 PT disorders associated with the expression or function of these enzymes -
 XX
 PS Example 4; Page 213-218; 336pp; Japanese.

XX The specification describes human protein kinase/protein phosphatases.
 CC The polypeptides are expected to participate in signal transduction
 CC in cells. The kinase phosphatases are connected with intracellular
 CC signalling pathways. Antisense oligonucleotides and compounds
 CC identified by screening (agonists or antagonists) can be used to
 CC treat human or animal disorders associated with the expression
 CC or function of the protein. In addition, the polypeptides may be used
 CC as target molecules for drug development. The present sequence
 CC represents a polypeptide, used in the course of the invention.

XX Sequence 648 AA;

Query Match 100.0%; Score 3413; DB 22; Length 648;
 Best Local Similarity 100.0%; Pred. No. 1.le-298;
 Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHIQAWKTSNGFGKDAVDFDGGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60
 DB 1 MEHIQAWKTSNGFGKDAVDFDGGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60
 QY 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFLLHHEHKGKARLDWNTDAAS 120
 DB 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFLLHHEHKGKARLDWNTDAAS 120
 QY 121 LIGEEQVDFLDHVPPLTHNFARKTFLKLAFCDICOKFLLNGFRCTCGYKFEHCSTKV 180
 DB 121 LIGEEQVDFLDHVPPLTHNFARKTFLKLAFCDICOKFLLNGFRCTCGYKFEHCSTKV 180
 QY 181 PTMCDVNSIRQLLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSOHRYSTPHFTTF 240
 DB 181 PTMCDVNSIRQLLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSOHRYSTPHFTTF 240
 QY 241 NTSSPSSBGLSQQRSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSSPNNL 300
 DB 241 NTSSPSSBGLSQQRSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSSPNNL 300
 QY 301 SPTGHSQKTPVPAQRERAPVSGTQEKNIIPRGQRDSSYYWETEASEVLMSTRIGSGSF 360
 DB 301 SPTGHSQKTPVPAQRERAPVSGTQEKNIIPRGQRDSSYYWETEASEVLMSTRIGSGSF 360
 QY 361 GTVYKGRWHGDVAVKILKVVDPTEQFOAFNEVAVLRKTRHVNILLFMGYMTKDNLAIV 420
 DB 361 GTVYKGRWHGDVAVKILKVVDPTEQFOAFNEVAVLRKTRHVNILLFMGYMTKDNLAIV 420
 QY 421 TQWCEGSLYKHLHVQETKFMQLIDIAQTQAGMDYLHAKNIIRHDMKSNIFLHEGL 480
 DB 421 TQWCEGSLYKHLHVQETKFMQLIDIAQTQAGMDYLHAKNIIRHDMKSNIFLHEGL 480
 QY 481 TVKIGDFGLAVTKRWGSGSQVEQPTGSLVMAPEVIRMQDNPPFSQSDVYSGVILYE 540
 DB 481 TVKIGDFGLAVTKRWGSGSQVEQPTGSLVMAPEVIRMQDNPPFSQSDVYSGVILYE 540
 QY 541 LMTGELPYSHINNRDQIIFMVGRGYASPDLSKKNCPKAMKRLVADCVKVKKEERPLFP 600
 DB 541 LMTGELPYSHINNRDQIIFMVGRGYASPDLSKKNCPKAMKRLVADCVKVKKEERPLFP 600
 QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPYF 648
 DB 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPYF 648

RESULT 12

RAG67619

ID AAG67619 standard; Protein; 648 AA.

XX AAG67619;

XX AC

XX 26-NOV-2001 (first entry)

XX Amino acid sequence of a human protein.

XX Human; protein kinase; protein phosphatase; signal transduction.

XX Homo sapiens.

XX WO200109316-A1.

XX 08-FEB-2001.

XX 28-JUL-2000; 2000WO-JP05061.

XX 29-JUL-1999; 99JP-0248036.

XX 18-OCT-1999; 99US-0159590.

XX 11-JAN-2000; 2000JP-0118776.

XX 17-FEB-2000; 2000US-0183322.

XX 02-MAY-2000; 2000JP-0183767.

XX 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;

XX Senoo C, Nezu J;

XX WPI: 2001-570286/64.

XX New genes encoding proteins with protein kinase/protein phosphatase

XX activity, useful in the diagnosis and treatment of diseases -

XX Example 4; Page 111-116; 233pp; Japanese.

XX The specification describes human protein kinase/protein phosphatases.

XX It is expected that the protein kinase/protein phosphatase gene

XX participates in signal transduction in cells. The protein

XX kinase/protein phosphatase polypeptides and polynucleotides are

XX useful for developing diagnostics and treatment agents for human

XX and animal diseases. The protein kinase/protein phosphatase polypeptides

XX are useful as target molecules in designing novel drugs. The protein

XX kinase/protein phosphatase polynucleotides are useful as a source of

XX probes and primers, which may be used to isolate homologous sequences.

XX The present sequence represents a human protein, which is used in the

XX course of the invention.

XX Sequence 648 AA;

XX Query Match 100.0%; Score 3413; DB 22; Length 648;

XX Best Local Similarity 100.0%; Pred. No. 1.le-298;

XX Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHIQAWKTSNGFGKDAVDFDGGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60

DB 1 MEHIQAWKTSNGFGKDAVDFDGGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60

QY 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFLLHHEHKGKARLDWNTDAAS 120

DB 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFLLHHEHKGKARLDWNTDAAS 120

QY 121 LIGEEQVDFLDHVPPLTHNFARKTFLKLAFCDICOKFLLNGFRCTCGYKFEHCSTKV 180

DB 121 LIGEEQVDFLDHVPPLTHNFARKTFLKLAFCDICOKFLLNGFRCTCGYKFEHCSTKV 180

QY 181 PTMCDVNSIRQLLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSOHRYSTPHFTTF 240

Db 181 PTMCDVMSNRQLLFPNSTIGSGVPALPFLTMRRRESVSRMPVSSQHRSTPHATF 240
Qy 241 NTSSPSEGLSQRORSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSPNL 300
Db 241 NTSSPSEGLSQRORSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSPNL 300
Qy 301 SPTGWSQKTPVPAQRERAPVSGTQEKNIIRPRGDRDSSYYWIEASEVYMLSTRIGSGSF 360
Db 301 SPTGWSQKTPVPAQRERAPVSGTQEKNIIRPRGDRDSSYYWIEASEVYMLSTRIGSGSF 360
Qy 361 GTVYKKGWHDGAVKILKVVDPPTPEQFOAFRNEVAVLKRTHVNIILFLWYTKDNLAIY 420
Db 361 GTVYKKGWHDGAVKILKVVDPPTPEQFOAFRNEVAVLKRTHVNIILFLWYTKDNLAIY 420
Qy 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQTQAGMDYLHAKNIIRHDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQTQAGMDYLHAKNIIRHDMKSNIFLHEGL 480
Qy 481 TVKIGDFGLATVKSRSWGSQVQPTGCVLWMAPEVIRMODNPFQSDVSYGIVLYE 540
Db 481 TVKIGDFGLATVKSRSWGSQVQPTGCVLWMAPEVIRMODNPFQSDVSYGIVLYE 540
Qy 541 LMTGELPYSHINNRDQIIFWVGGRGYASPDLSKLYKNCPRAMKRLVADCVKKKEERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFWVGGRGYASPDLSKLYKNCPRAMKRLVADCVKKKEERPLFP 600
Qy 601 QILSSIELLQHSPLKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
Db 601 QILSSIELLQHSPLKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 13
ABB76179
ID ABB76179 standard; Protein: 648 AA.
AC ABB76179;
XX
XX
DT 22-JUL-2002 (first entry)
DE Human protein kinase C-Raf.
KW C-Raf; protein kinase; human; antitumour; antidiabetic;
KW antinflammatory; vasotropic; vulnery; antithrombotic;
KW neuroprotective; nootropic; cerebroprotective; antipsoriatic;
KW antiarthritic; signal transduction; gene therapy.
XX
OS Homo sapiens.
XX
XX WO200226246-A2.
XX
XX
PD 04-APR-2002.
PF 28-SEP-2001; 2001WO-EP11282.
XX
XX 29-SEP-2000; 2000EP-0121490.
XX
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
XX
PI Hatzopoulos A, Hautmann M, Herbst M, Gelshauser A, Schoch J;
XX
XX WPI; 2002-402033/43.
DR N-PSDB; ABL57050.
XX
XX Composition for treating or preventing pathological conditions in which
XX endothelial cells are involved or affected e.g. diabetes, inflammation,
PT psoriasis, has Raf protein, polynucleotide, or modulators of the
PT protein -
XX
XX Claim 1; Page 62-64; 64pp; English.
PS
XX
XX The present sequence is the protein sequence of human C-Raf, a
CC protein kinase involved in signal transduction cascades. The

CC invention provides pharmaceutical compositions (PCs) comprising
CC a polynucleotide encoding a Raf protein, especially A-Raf, B-Raf
CC or C-Raf, in particular B-Raf, a vector comprising A-Raf, B-Raf
CC expressing the polynucleotide, host cells genetically engineered
CC with the polynucleotide or vector, a polypeptide encoded by the
CC polynucleotide, agonists or antagonists of the polypeptide and the
CC methods of identifying them, and diagnostic compositions. The PCs
CC are used to prevent or treat a condition in which endothelial
CC cells are involved or affected, by inhibiting or promoting
CC angiogenesis, modulating the permeability of the blood-brain
CC barrier, or by blocking or enhancing cell migration during
CC angiogenesis or tissue remodelling. The PCs are useful for treating
CC or preventing tumours, diabetic retinopathy, chronic inflammatory
CC disease, restenosis, cardiomyopathy, inflammation, atherosclerosis,
CC stroke or myocardial infarction, for promoting wound healing,
CC enhancing circulation, inhibiting tumour development especially
CC metastasis, for treating pathophysiological conditions or injury of
CC the vascular wall, Alzheimer's disease, and for preventing
CC coagulation or fibrin deposition in the vessels (all claimed). A
CC claimed diagnostic composition comprising a Raf polynucleotide,
CC vector, host cell, polypeptide or antibody, is useful for diagnosing
CC a pathological condition or a susceptibility to a pathological
CC condition in a subject, by determining the expression level of Raf
CC in a sample.
XX
SQ Sequence 648 AA;
Query Match 100.0%; Score 3413; DB 23; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.1e-398;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEHIOGAWKTTISNGFGFKDAVFDGSSCISPIVQFGYQRRASDDGKLTDSKTSNIRV 60
Db 1 MEHIOGAWKTTISNGFGFKDAVFDGSSCISPTIVQFGYQRRASDDGKLTDSKTSNIRV 60
Qy 61 FLPNKQRTVNVNRGMSLHDCMLKALKVGRLOPECCAVFLLHGHKKGKARLDNTDAAS 120
Db 61 FLPNKQRTVNVNRGMSLHDCMLKALKVGRLOPECCAVFLLHGHKKGKARLDNTDAAS 120
Qy 121 LIGELQVDFLDHVPLTTHNFARKTFLKAFDCICQKFLNGFCQTCGYKFHEHCSTKV 180
Db 121 LIGELQVDFLDHVPLTTHNFARKTFLKAFDCICQKFLNGFCQTCGYKFHEHCSTKV 180
Qy 181 PTMCDVMSNRQLLFPNSTIGSGVPALPFLTMRRRESVSRMPVSSQHRSTPHATF 240
Db 181 PTMCDVMSNRQLLFPNSTIGSGVPALPFLTMRRRESVSRMPVSSQHRSTPHATF 240
Qy 241 NTSSPSEGLSQRORSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSPNL 300
Db 241 NTSSPSEGLSQRORSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSALSSPNL 300
Qy 301 SPTGWSQKTPVPAQRERAPVSGTQEKNIIRPRGDRDSSYYWIEASEVYMLSTRIGSGSF 360
Db 301 SPTGWSQKTPVPAQRERAPVSGTQEKNIIRPRGDRDSSYYWIEASEVYMLSTRIGSGSF 360
Qy 361 GTVYKKGWHDGAVKILKVVDPPTPEQFOAFRNEVAVLKRTHVNIILFLWYTKDNLAIY 420
Db 361 GTVYKKGWHDGAVKILKVVDPPTPEQFOAFRNEVAVLKRTHVNIILFLWYTKDNLAIY 420
Qy 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQTQAGMDYLHAKNIIRHDMKSNIFLHEGL 480
Db 421 TQWCEGSSLYKHLHVQETKFMQFQIDIAQTQAGMDYLHAKNIIRHDMKSNIFLHEGL 480
Qy 481 TVKIGDFGLATVKSRSWGSQVQPTGCVLWMAPEVIRMODNPFQSDVSYGIVLYE 540
Db 481 TVKIGDFGLATVKSRSWGSQVQPTGCVLWMAPEVIRMODNPFQSDVSYGIVLYE 540
Qy 541 LMTGELPYSHINNRDQIIFWVGGRGYASPDLSKLYKNCPRAMKRLVADCVKKKEERPLFP 600
Db 541 LMTGELPYSHINNRDQIIFWVGGRGYASPDLSKLYKNCPRAMKRLVADCVKKKEERPLFP 600
Qy 601 QILSSIELLQHSPLKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
Db 601 QILSSIELLQHSPLKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 14

AAG80183

ID AAG80183 standard; Protein; 648 AA.

XX AAG80183;

XX 21-JAN-2002 (first entry)

XX Human c-raf-1 protein.

XX Oncogene; c-raf-1; human; MEK1; MEK kinase; raf-binding; cytostatic;

XX mitogen activated and extracellular stimuli regulated kinase;

XX gene therapy; NF-kB suppression; tumour cell proliferation;

XX NF-kB-mediated signal cascade.

XX Homo sapiens.

XX WO200179501-A2.

XX 25-OCT-2001.

XX 17-APR-2001; 2001WO-DE01518.

XX 14-APR-2000; 2000DE-1020138.

XX (RAPP/) RAPP U R.

XX (WIRTH/) WIRTH T.

XX Rapp UR, Wirth T;

XX WPI; 2002-017617/02.

XX N-PSDB; RAI68698.

XX New nucleic acid encoding partial raf sequence, useful for identifying compounds that block binding of raf to its activating kinase as potential anticancer agents -

XX Disclosure; Fig 10b-f; 66pp; German.

XX This invention describes a novel nucleic acid (I) that: (i) encodes at least one raf partial sequence containing a MEK1 (mitogen activated and extracellular stimuli regulated (MEK) kinase) binding site; (ii) encodes at least one partial sequence of MEK1 containing a raf binding site; (iii) is a silent mutation of (i) or (ii); or (iv) hybridizes to (i)-(iii). The products of the invention have cytostatic activity and can be used for gene therapy. The products also suppress NF-kB activation resulting in inhibition of tumour cell proliferation or transformation. (I), or proteins/peptides encoded by them, are useful for identifying compounds that block binding of raf to MEK1. These compounds, optionally where expressed from gene therapy vectors, are useful in human or veterinary medicine for treatment of tumors. Antisense sequences, or ribozymes, that bind to (I) are used to inhibit MEK1 activation. Also nucleic acid (I') encoding at least a part of raf (or its silent mutations or hybridizing sequences) is used to examine interaction of encoded proteins with activation of the NF-kB-mediated signal cascade and to screen for inhibitors of cell transformation by raf-mediated activation of NF-kB. This sequence represents the human c-raf-1 oncogene described in the method of the invention.

XX Sequence 648 AA;

Query Match 100.0%; Score 3413; DB 23; Length 648;

Best Local Similarity 100.0%; Pred. No. 1.1e-298;

Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHIQGAWKTIISNGFGKDAVDFGSSCISPTIVQFGYQRRASDDGLTDPKTSNTIRV 60

DB 1 MEHIQGAWKTIISNGFGKDAVDFGSSCISPTIVQFGYQRRASDDGLTDPKTSNTIRV 60

QY 61 FLPNKQRTVVNVRNGMSLHCLMKALKVRGLQPECCAVFRLHHEHGKKARLDWNTDAAS 120

DB 61 FLPNKQRTVVNVRNGMSLHCLMKALKVRGLQPECCAVFRLHHEHGKKARLDWNTDAAS 120

QY 121 LIGEELOVDFLDHVPLTTHNFARKFTFLKAFCDICOKFLLNGFRFCOTCGYKPFHEHCSTKV 180

DB 121 LIGEELOVDFLDHVPLTTHNFARKFTFLKAFCDICOKFLLNGFRFCOTCGYKPFHEHCSTKV 180

QY 181 PTMCDWSNIROQLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRVSTPHATF 240

DB 181 PTMCDWSNIROQLLFPNSTIGDSGVPALPSLTMRMRRESVSRMPVSSQHRVSTPHATF 240

QY 241 NTSSPSSEGLSQORQRSTSTPNVHVSTTLPVDSRMIEDAIRSHSESASPSALSSPNNL 300

DB 241 NTSSPSSEGLSQORQRSTSTPNVHVSTTLPVDSRMIEDAIRSHSESASPSALSSPNNL 300

QY 301 SPTGWSQKTPVPAQREAPVSGTQKKNIRPGORDSSYYWEIEASEVMLSTRIGSGSF 360

DB 301 SPTGWSQKTPVPAQREAPVSGTQKKNIRPGORDSSYYWEIEASEVMLSTRIGSGSF 360

QY 361 GTVYKGKWHGDVAVKILKVVDPTPEQFAFRNEVAVLRKTRHVNILLFPMGYTKDNLAIV 420

DB 361 GTVYKGKWHGDVAVKILKVVDPTPEQFAFRNEVAVLRKTRHVNILLFPMGYTKDNLAIV 420

QY 421 TWCCEGSSLYKHLHVQETKFMQLIDTARQTAQGM DYLHAKNIITHRDMKSNIFLHEGL 480

DB 421 TWCCEGSSLYKHLHVQETKFMQLIDTARQTAQGM DYLHAKNIITHRDMKSNIFLHEGL 480

QY 481 TVKIGDFGLATVKSRSWSSQVEQPTGTVLWNAPEVIRMQDNPNPFSQSDVTSYGIVLYE 540

DB 481 TVKIGDFGLATVKSRSWSSQVEQPTGTVLWNAPEVIRMQDNPNPFSQSDVTSYGIVLYE 540

QY 541 LMTGELPYSHINNROQIIFMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600

DB 541 LMTGELPYSHINNROQIIFMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600

QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

DB 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 15

AAB70297 standard; Protein; 668 AA.

XX AAB70297;

XX 10-MAY-2001 (first entry)

XX Raf-caax fusion protein.

XX Raf; ras; vector; tumour; arthritis; retinopathy; angioplasty.

XX Homo sapiens.

XX WO200112210-A1.

XX 22-FEB-2001.

XX 11-AUG-2000; 2000WO-US21842.

XX 13-AUG-1999; 99US-0148924.

XX 05-JUL-2000; 2000US-0215951.

XX (SCRI) SCRIPPS RES INST.

XX Hood J, Elliceiri B, Cheresh DA;

XX WPI; 2001-202826/20.

XX Composition for modulating angiogenesis and treating rheumatoid arthritis and restenosis comprises Raf protein or viral or non-viral gene transfer vector containing nucleic acid encoding for Raf or Ras protein -

```
XX PS Disclosure; Fig 15; 102pp; English.
XX
CC The present invention relates to a composition with a
CC Raf protein or a viral or non-viral gene transfer vector containing
CC a nucleic acid encoding for a Raf or Ras protein. The Raf
CC protein optionally has kinase activity and the Ras protein has
CC angiogenesis modulating activity. The invention is useful for
CC modulating angiogenesis in a tissue which has poor or abnormal
CC circulation, in a tissue which is a solid tumor or solid tumour
CC metastasis, in an inflamed tissue associated with arthritis or
CC rheumatoid arthritis, in a retinal tissue associated with retinopathy,
CC diabetic retinopathy or macular degeneration, or in a tissue which is
CC at the site of coronary angioplasty associated with restenosis.
XX
SQ Sequence 668 AA;
Query Match 100.0%; Score 3413; DB 22; Length 668;
Best Local Similarity 100.0%; Pred. No. 1.1e-298;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHIOGAWKTIISNGFGKDAVDFGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60
Db 1 MEHIOGAWKTIISNGFGKDAVDFGSSCISPTIVQFGYQRRASDDGKLTDPKTSNTIRV 60
QY 61 FLPNKQRTVVNVVANGSLHDCLMKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAAS 120
Db 61 FLPNKQRTVVNVVANGSLHDCLMKALKVRGLQPECCAVFRLLEHKGKARLDWNTDAAS 120
QY 121 LIGEEQLQVDFLDHVLTTHNFARKTFLKLAFCDDICOKFLNGFRQTCGYKFEHCSTKV 180
Db 121 LIGEEQLQVDFLDHVLTTHNFARKTFLKLAFCDDICOKFLNGFRQTCGYKFEHCSTKV 180
QY 181 PTMCDWSNIRQLLLFPNSTIGDSGVPALPSLTMRMRRESVSMPVSSQHYSTPHATTF 240
Db 181 PTMCDWSNIRQLLLFPNSTIGDSGVPALPSLTMRMRRESVSMPVSSQHYSTPHATTF 240
QY 241 NTSSPSSGSLSORQSTSTPNVHVSTTLPVDSRMIEDAIRSHSESASPSALSSPNL 300
Db 241 NTSSPSSGSLSORQSTSTPNVHVSTTLPVDSRMIEDAIRSHSESASPSALSSPNL 300
QY 301 SPTGWSQKTPVPAQERAPVSGTQEKNIIRPRGQDSSYYWEIEASEVMLSTRIGSGSF 360
Db 301 SPTGWSQKTPVPAQERAPVSGTQEKNIIRPRGQDSSYYWEIEASEVMLSTRIGSGSF 360
QY 361 GTVYKKGWHDVAVKILKVVDPTPEQFAFRNEVAVLRKTRHVNILLFMGYMTKDNLAIV 420
Db 361 GTVYKKGWHDVAVKILKVVDPTPEQFAFRNEVAVLRKTRHVNILLFMGYMTKDNLAIV 420
QY 421 TQCEGSSLYKHLHVQETKFMQLDIDARQTAQGM DYLHAKNIIHRDMKSNFIHLEGL 480
Db 421 TQCEGSSLYKHLHVQETKFMQLDIDARQTAQGM DYLHAKNIIHRDMKSNFIHLEGL 480
QY 481 TVKIGDFGLATVKRSWGSQQVEQPTGSLWMAPEVIRMODNNPFQSDVYSYGVLYE 540
Db 481 TVKIGDFGLATVKRSWGSQQVEQPTGSLWMAPEVIRMODNNPFQSDVYSYGVLYE 540
QY 541 LMTGELPYSHINNRODIIIFWVGRYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
Db 541 LMTGELPYSHINNRODIIIFWVGRYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTILTTSPRLPVF 648
Db 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTILTTSPRLPVF 648
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Search completed: July 9, 2003, 09:44:55
Job time : 44 secs

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OM protein - protein search, using sw model

Run on: July 9, 2003, 09:37:02 ; Search time 26 Seconds
(without alignments)
1033.718 Million cell updates/sec

Title: US-09-637-302C-2

Perfect score: 3413

Sequence: 1 MEHQGAWKTSNGFGKDA.....AHTEDINACTLTSPRLPVF 648

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3413	100.0	648	1 KRAF_HUMAN	P04049 homo sapien
2	3349	98.1	648	1 KRAF_RAT	P11345 rattus norv
3	3249.5	95.2	647	1 KMIL_CHICK	P05625 gallus gall
4	2885	84.5	638	1 KRAF_XENLA	P09560 xenopus lae
5	1893.5	55.5	606	1 KRAA_PIG	O19004 sus scrofa
6	1891.5	55.4	604	1 KRAA_RAT	P14056 rattus norv
7	1890.5	55.4	604	1 KRAA_MOUSE	P04627 mus musculu
8	1889.5	55.4	606	1 KRAA_HUMAN	P10398 homo sapien
9	1888.5	55.3	380	1 KMIL_AVIIMH	P00531 avian retro
10	1825	53.5	765	1 KRAF_HUMAN	P15056 homo sapien
11	1814	53.1	806	1 RMIL_CHICK	Q04982 gallus gall
12	1814	53.1	807	1 RMIL_COTJA	P34908 coturnix co
13	1654	48.5	323	1 KRAF_MSV36	P00532 murine sarc
14	1360	39.8	781	1 KRAF_DRONE	P11346 drosophila
15	1336	39.1	450	1 RMIL_AVEVR	P27966 avian rous-
16	1327.5	38.9	367	1 RMIL_AVIIL	P10533 avian retro
17	1277	37.4	328	1 KRAF_MOUSE	P28028 mus musculu
18	1121.5	32.9	813	1 KRAF_CAEEL	Q07292 caenorhabdi
19	455.5	13.3	821	1 CTRI_ARATH	Q05609 arabidopsis
20	412.5	12.1	568	1 SRC_AVISS	P14084 avian sarco
21	407	11.9	528	1 YES_AVISY	P00527 avian sarco
22	404	11.8	505	1 FRK_HUMAN	P2685 homo sapien
23	404	11.8	541	1 YES_CHICK	P09324 gallus gall
24	403	11.8	536	1 FYN_HUMAN	P06241 homo sapien
25	403	11.8	536	1 FYN_XENLA	P13406 xenopus lae
26	402	11.8	536	1 FYN_XIPHE	P27446 xiphophorus
27	401.5	11.8	505	1 SRK1_SPOLA	P42685 spongilla 1
28	401	11.7	544	1 YES_XIPHE	P27447 xiphophorus
29	397	11.6	535	1 SRC_HUMAN	P12931 homo sapien
30	396	11.6	539	1 YES_CANFA	Q28923 canis famil
31	395	11.6	532	1 SRC_CHICK	P00523 gallus gall
32	395	11.6	543	1 YES_HUMAN	P07947 homo sapien
33	395	11.6	557	1 SRC_AVISI	P14085 avian sarco

RESULT 1	KRAF_HUMAN	STANDARD;	PRT;	648 AA.
34	395	11.6	587	1 SRC_AVIS2
35	394	11.5	540	1 SRC_MOUSE
36	394	11.5	541	1 YES_MOUSE
37	393.5	11.5	334	1 SRK3_SPOLA
38	393	11.5	531	1 SRC2_XENLA
39	393	11.5	535	1 SRC_RAT
40	392	11.5	531	1 SRC1_XENLA
41	391.5	11.5	983	1 EPA3_HUMAN
42	391	11.5	507	1 LCK_CHICK
43	388	11.4	533	1 FYN_MOUSE
44	388	11.4	535	1 YRK_CHICK
45	388	11.4	537	1 YES_XENLA

ALIGNMENTS

AC P04049; 01-NOV-1986 (Rel. 03, Created)

DT 01-NOV-1986 (Rel. 03, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE RAF proto-oncogene serine/threonine-protein kinase (EC 2.7.1.-)

DE (RAF-1) (C-RAF).

GN RAF1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RX MEDLINE=86120351; PubMed=3003687;

RA Bonner T.I., Oppermann H., Seeburg P., Kerby S.B., Gunnell M.A., Young A.C., Rapp U.R.;

RA "The complete coding sequence of the human raf oncogene and the corresponding structure of the c-raf-1 gene.";

RL Nucleic Acids Res. 14:1009-1015(1986).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Pancreas;

RA Strausberg R.;

RN Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

RN [3]

RP PHOSPHORYLATION.

RX MEDLINE=99039505; PubMed=9823899;

RA King A.J., Sun H., Diaz B., Barnard D., Miao W., Bagrodia S., Marshall M.S.;

RA "The protein kinase Pak3 positively regulates Raf-1 activity through phosphorylation of serine 338.";

RL Nature 396:180-183(1998).

RN [4]

RP ERATUM.

RA King A.J., Sun H., Diaz B., Barnard D., Miao W., Bagrodia S., Marshall M.S.;

RA Nature 406:439-439(2000).

RN [5]

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 51-131.

RX MEDLINE=95312074; PubMed=7791872;

RA Nassar N., Horn G., Herrmann C., Scherer A., McCormick F., Wittinghofer A.;

RA "The 2.2 A crystal structure of the Ras-binding domain of the serine/threonine kinase c-Raf1 in complex with Rap1A and a GTP analogue.";

RL Nature 375:554-560(1995).

RN [6]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 56-131.

RX MEDLINE=96313130; PubMed=8756332;

RA Nassar N., Horn G., Herrmann C., Block C., Janknecht R., Wittinghofer A.;

RA "Ras/Rap effector specificity determined by charge reversal.";

RL Nat. Struct. Biol. 3:723-729(1996).

RN RP STRUCTURE BY NMR OF 55-132.
 RX MEDLINE=95284022; PubMed=7766599;
 RA Emerson S.D., Madison V.S., Palermo R.E., Waugh D.S., Scheffler J.E.,
 RA Tsao K.L., Kiefer S.E., Liu S.P., Fry D.C.;
 RT "Solution structure of the Ras-binding domain of c-Raf-1 and
 RT identification of its Ras interaction surface.";
 RL Biochemistry 34:6911-6918(1995).
 RN RP [8]
 RN RP STRUCTURE BY NMR OF 136-187.
 RX MEDLINE=96323218; PubMed=8710867;
 RA Mott H.R., Carpenter J.W., Zhong S., Ghosh S., Bell R.M.,
 RA Campbell S.L.;
 RT "The solution structure of the Raf-1 cysteine-rich domain: a novel
 RT ras and phospholipid binding site.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:8312-8317(1996).
 CC -1- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS FROM
 CC THE CELL MEMBRANE TO THE NUCLEUS. PART OF THE RAS-DEPENDENT
 CC SIGNALING PATHWAY FROM RECEPTORS TO THE NUCLEUS.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MIL/RAF SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC BINDING DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; X03484; CAA27204.1; --
 DR EMBL; BC018119; AAH18119.1; --
 DR PIR; A00637; TVHUF6.
 DR PDB; 1FAQ; 27-JAN-97.
 DR PDB; 1FAR; 27-JAN-97.
 DR PDB; 1FEA; 20-JUN-96.
 DR PDB; 1GUA; 11-JAN-97.
 DR Genew; HGNC:9829; RAF1.
 DR MIM; 164760; --
 DR InterPro; IPR002219; DAG_PE-bind.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003116; RBD.
 DR InterPro; IPR004040; STY_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00130; DAG_PE-bind; 1.
 DR Pfam; PF02196; RBD; 1.
 DR PRINTS; PR00008; DAGPEDOMAIN.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00109; CI; 1.
 DR SMART; SM00455; RBD; 1.
 DR SMART; SM00221; STYKC; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;
 KW ATP-binding; Phorbol-ester binding; Phosphorylation; 3D-structure.
 FT DOMAIN 139 184 PHORBOL-ESTER AND DAG BINDING.
 FT DOMAIN 349 609 PROTEIN KINASE.
 FT NP_BIND 355 363 ATP (BY SIMILARITY).
 FT BINDING 375 375 ATP (BY SIMILARITY).
 FT ACT_SITE 468 468 BY SIMILARITY.
 FT MOD_RES 338 338 PHOSPHORYLATION (BY PAK2 AND PAK3).
 SQ SEQUENCE 648 AA; EF821B5349711BC3 CRC64;
 Query Match 100.0%; Score 3413; DB 1; Length 648;
 Best Local Similarity 100.0%; Pred. No. 3.6e-223;
 Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTQAGKWTISNGFGKDAVDFGSSCISPIIVQFGYQRRASDDGKLTDPKTSNTIRV 60
 DB 1 MEHTQAGKWTISNGFGKDAVDFGSSCISPIIVQFGYQRRASDDGKLTDPKTSNTIRV 60
 QY 61 FLPNKQRTVNVNRNGMSLHDCMLKALKVRGLQPECCAVFLLHKGKARLDWNTDAAS 120
 DB 61 FLPNKQRTVNVNRNGMSLHDCMLKALKVRGLQPECCAVFLLHKGKARLDWNTDAAS 120
 QY 121 LIGELQVDFLDHVPLTTHNFARKTFLKAFCDICQKFLNGLFGFCQTCGKFEHCSTKV 180
 DB 121 LIGELQVDFLDHVPLTTHNFARKTFLKAFCDICQKFLNGLFGFCQTCGKFEHCSTKV 180
 QY 181 PTMCVDMSNIRQLLLFPNSTIGDSGVPALPSLTWRRMRRESVSRMPVSSQHRYSPTPHTFF 240
 DB 181 PTMCVDMSNIRQLLLFPNSTIGDSGVPALPSLTWRRMRRESVSRMPVSSQHRYSPTPHTFF 240
 QY 241 NTSSPSSGSLSQQRSTSTPNVHMVSTTLTPVDSRMEDAIRSHSESASPSALSSSPNNL 300
 DB 241 NTSSPSSGSLSQQRSTSTPNVHMVSTTLTPVDSRMEDAIRSHSESASPSALSSSPNNL 300
 QY 301 SPTGWSQPKTPVPAQRRAPVSGTQENKIRPGQRDSSYYWEIEASEVMLSTRIGSGSF 360
 DB 301 SPTGWSQPKTPVPAQRRAPVSGTQENKIRPGQRDSSYYWEIEASEVMLSTRIGSGSF 360
 QY 361 GTVYKGWHGQVAVKILKVVDPTEQQAQFNEAVLRKTHVNVILLFMGYMTKDNLAIV 420
 DB 361 GTVYKGWHGQVAVKILKVVDPTEQQAQFNEAVLRKTHVNVILLFMGYMTKDNLAIV 420
 QY 421 TQWCEGSSLYKHLHVQETKFMFQIDIAQTQAGMDYLHAKNIHHRDKSNINFLHEGL 480
 DB 421 TQWCEGSSLYKHLHVQETKFMFQIDIAQTQAGMDYLHAKNIHHRDKSNINFLHEGL 480
 QY 481 TVKIGDFGLATVKSNGSGSQVEOPTGSLVMAPEVIRMQDNNPFSQSDYSYGIYLYE 540
 DB 481 TVKIGDFGLATVKSNGSGSQVEOPTGSLVMAPEVIRMQDNNPFSQSDYSYGIYLYE 540
 QY 541 LMTGELPYSHNNRDOIFFMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
 DB 541 LMTGELPYSHNNRDOIFFMVGRGYASPDLSKLYKNCPKAMKRLVADCVKVKKEERPLFP 600
 QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
 DB 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648
 RESULT 2
 KRAF_RAT ID KRAF_RAT STANDARD; PRG; 648 AA.
 AC P11345;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DT RAF proto-oncogene serine/threonine-protein kinase (EC 2.7.1.-)
 DE (RAF-1) (C-RAF).
 GN RAF1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=87172791; PubMed=3550433;
 RA Ishikawa F., Takaku F., Nagao M., Sugimura T.;
 RT "Rat c-raf oncogene activation by a rearrangement that produces a
 RL fused protein.";
 RN [2]
 RN Mol. Cell. Biol. 7:1226-1232(1987).
 RX STRUCTURE BY NMR OF 51-131.
 RA MEDLINE=99134400; PubMed=9931261;
 RA Terada T., Ito Y., Shirouzu M., Tateo M., Hashimoto K., Kigawa T.,
 RA Ebisuzaki T., Takio K., Shibata T., Yokoyama S., Smith B.O.,
 RA Laue E.D., Cooper J.A.;
 RT "Nuclear magnetic resonance and molecular dynamics studies on the

interactions of the Ras-binding domain of Raf-1 with wild-type and mutant Ras proteins.;

J. Mol. Biol. 286:219-232(1999).

-1- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS FROM THE CELL MEMBRANE TO THE NUCLEUS. PART OF THE RAS-DEPENDENT SIGNALING PATHWAY FROM RECEPTORS TO THE NUCLEUS.

-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MIL/RAF SUBFAMILY.

-1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG BINDING DOMAIN.

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EMBL; M15427; AAA42001.1; .

PIR; A26126; TVTRF.

PIR; B26126; TVTRF.

PDB; 1RRB; 30-MAR-99.

InterPro; IPR002219; DAG_PE-bind.

InterPro; IPR000719; Euk_pkinase.

InterPro; IPR003116; RBD.

InterPro; IPR004040; STY_pkinase.

InterPro; IPR002290; Ser_thr_pkinase.

Pfam; PF00130; DAG_PE-bind; 1.

Pfam; PF02196; RBD; 1.

PRINTS; PR00008; DAGPEDOMAIN.

ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00109; Cl; 1.

SMART; SM00455; RBD; 1.

SMART; SM00221; STYKc; 1.

PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.

PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

Transferrase; Serine/threonine-protein kinase; Proto-oncogene; Zinc; ATP-binding; Phosphorylation; Phorbol-ester binding; 3D-structure.

DOMAIN 139 184 PHORBOL-ESTER AND DAG BINDING.

FT 349 509 PROTEIN KINASE.

FT NP_BIND 355 363 ATP (BY SIMILARITY).

FT BINDING 375 375 ATP (BY SIMILARITY).

FT ACT_SITE 468 468 BY SIMILARITY.

FT MOD_RES 499 499 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

SQ SEQUENCE 648 AA; 72928 MW; 59AFB5975064193E CRC64;

Query Match 98.18; Score 3349; DB 1; Length 648;

Best Local Similarity 98.34; Pred. No. 7.6e-219;

Matches 637; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 MEHLOGAWKTSNGFGKDAVFDGSSCISPTIVQFGYQRRASDGLKTOPSKTSNIRV 60

DB 1 MEHLOGAWKTSNGFGKDAVFDGSSCISPTIVQFGYQRRASDGLKTOPSKTSNIRV 60

QY 61 FLPNKQRTVNVNRGMSLHDCMLKALVRLQPECCAVFLLHKKKARLDWNTDAAS 120

DB 61 FLPNKQRTVNVNRGMSLHDCMLKALVRLQPECCAVFLLHKKKARLDWNTDAAS 120

QY 121 LIGELQVDFLDHVLTHNFARKTFLKAFCDICQKFLNGFRQCOTCGYKFHEHCSTKV 180

DB 121 LIGELQVDFLDHVLTHNFARKTFLKAFCDICQKFLNGFRQCOTCGYKFHEHCSTKV 180

QY 181 PTMCVDMSNRQLLFPNSTIGDSGVPALPSLTHRRMRRESVSRMPVSSQHYSTPHAF 240

DB 181 PTMCVDMSNRQLLFPNSTIGDSGVPALPSLTHRRMRRESVSRMPVSSQHYSTPHAF 240

QY 241 NTSSPSSEGSLSQRQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSSALSSSPNNL 300

Db 241 NTSSPSSEGSLSQRQSTSTPNVHMVSTTLPVDSRMIEDAIRSHSESASPSSALSSSPNNL 300

QY 301 SPTGWSQKTPVPAQERAPVSGTQKKNIRPGQDSSYYWIEASEVNLSTRIGSGSF 360

DB 301 SPTGWSQKTPVPAQERAPVSGTQKKNIRPGQDSSYYWIEASEVNLSTRIGSGSF 360

QY 361 GTVYKGNWGDVAVKILKVVDPPTPEQFAFRNEVAVLRKTRHVNILFELMGYTKDNLAI 420

DB 361 GTVYKGNWGDVAVKILKVVDPPTPEQFAFRNEVAVLRKTRHVNILFELMGYTKDNLAI 420

QY 421 TQCEGSSLYKHLHVQETKFMQFQDLIDIAQAGMDYLHAKNIIRDMSNNIFLHEGL 480

DB 421 TQCEGSSLYKHLHVQETKFMQFQDLIDIAQAGMDYLHAKNIIRDMSNNIFLHEGL 480

QY 481 TVKIGDFGLATVKSRWSGSOQVQPTGSGVLMWMAPEVIRMODNNPRFSQSDVTSYGIVLYE 540

DB 481 TVKIGDFGLATVKSRWSGSOQVQPTGSGVLMWMAPEVIRMODNNPRFSQSDVTSYGIVLYE 540

QY 541 LMTGELPYSHINNROQIIFMVGRGYASPOLSKLYKNCCKAMKRLVADCVKVKKEERPLFP 600

DB 541 LMTGELPYSHINNROQIIFMVGRGYASPOLSKLYKNCCKAMKRLVADCVKVKKEERPLFP 600

QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

DB 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPRLPVF 648

RESULT 3

KMIL_CHICK

ID KMIL_CHICK STANDARD; PRT; 647 AA.

AC P05625;

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE MIL proto-oncogene serine/threonine-protein kinase (EC 2.7.1.37).

GN C-MIL.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Erythroblast;

RX MEDLINE=88217299; PubMed=3285296;

RA Koenen M., Sippel A.E., Trachmann C., Bister K.;

RT "Primary structure of the chicken c-mil protein. Identification of

RT domains shared with or absent from the retroviral v-mil protein.";

NL Oncogene 2:179-185(1988).

CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC MIL/RAF SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG BINDING DOMAIN.

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EMBL; X07017; CAA30069.1; .

PIR; S00644; S00644.

HSSP; P04049; 1FAR.

InterPro; IPR002219; DAG_PE-bind.

InterPro; IPR000719; Euk_pkinase.

InterPro; IPR003116; RBD.

InterPro; IPR004040; STY_pkinase.

InterPro; IPR002290; Ser_thr_pkinase.

Pfam; PF00069; pkinase; 1.

Pfam; PF00130; DAG_PE-bind; 1.

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DR Pfam; PF02196; RBD; 1.
DR PRINTS; PS00008; DAGPEDOMAIN.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00455; RBD; 1.
DR SMART; SM00221; STYK; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;
KW ATP-binding; Phorbol-ester binding.
FT DOMAIN 139 184 PHORBOL-ESTER AND DAG BINDING.
FT NP_BIND 349 609 PROTEIN KINASE.
FT BINDING 355 363 ATP (BY SIMILARITY).
FT BINDING 375 375 ATP (BY SIMILARITY).
FT ACT_SITE 468 468 BY SIMILARITY.
SQ SEQUENCE 647 AA; 73124 MW; 8E1443667312DFC0 CRC64;

Query Match 95.2%; Score 3249.5; DB 1; Length 647;
Best Local Similarity 94.6%; Pred. No. 4e-212;
Matches 613; Conservative 20; Mismatches 14; Indels 1; Gaps 1;

QY 1 MEHIQAWKTIINGFGFKDAVFDGSSCISPTIVQFGYORRASDDGKLTDPKTSNTIRV 60
DB 1 MEHIQAWKTIINGFGKDSVDFGNCISPTIVQFGYORRASDDGKISDTKTSNTIRV 60
QY 61 FLFNKQRTVVNRVNGSLHDCMLKALKVRLGLOPECCAVFLRLEHKGKARLDWNTDAAS 120
DB 61 FLFNKQRTVVNRVNGSLHDCMLKALKVRLGLOPECCAVFLRLEHKGKARLDWNTDAAS 120
QY 121 LIGEELOVDFLHVPLTHNFARKTFLKLAFCIDCKQLFLLNGFRQTCGKPFHEHCSTKV 180
DB 121 LIGEELOVDFLHVPLTHNFARKTFLKLAFCIDCKQLFLLNGFRQTCGKPFHEHCSTKV 180
QY 181 PTMCVDSNIRQLLPNPNSTIGSGVPALPSTMTMRBESVSRVPSQHRVSTPHATF 240
DB 181 PTMCVDSNIRQLLPNPNSTIGSGVPALPSTMTMRBESVSRVPSQHRVSTPHATF 240
QY 241 NTSPPSEGLSQORSTSTPNVHMVSTLTPVDSRMIEDAIRSHSESAPSSALSSPNNL 300
DB 241 NTSPPSEGLSQORSTSTPNVHMVSTLTPVDSRMIEDAIRSHSESAPSSALSSPNNM 300
QY 301 SPTGWSQKTPPAQERAPVSGTQKKNIRPRGQDSSYYWEIEASEVWMLSTRIGSGSF 360
DB 301 SPTGWSQKTPPAQERAPVSGTQKKNIRPRGQDSSYYWEIEASEVWMLSTRIGSGSF 360
QY 361 GTVYKKGWGDVAVKILKVVDPTPEQFAFRNEVAVLRKTRHVNILLFPGYMTKDLNLAIV 420
DB 361 GTVYKKGWGDVAVKILKVVDPTPEQFAFRNEVAVLRKTRHVNILLFPGYMTKDLNLAIV 420
QY 421 TQWCEGSSLYKHLHVQETKFMQLDIAQTAQGMVYLHAKNIITHROMKSNIFLHBL 480
DB 421 TQWCEGSSLYKHLHVQETKFMQLDIAQTAQGMVYLHAKNIITHROMKSNIFLHBL 480
QY 481 TVKIGDFGLATVKSRSSGQVQEPGVSILWMAPEVIRMODNPNFSFQSDVYSYGLVLYE 540
DB 481 TVKIGDFGLATVKSRSSGQVQEPGVSILWMAPEVIRMODNPNFSFQSDVYSYGLVLYE 540
QY 541 LMTGELPYSHINRQDIIFWVGYSASPDLSKLYKNCPRKARLVADCVKKYKEERPLFP 600
DB 541 LMTGELPYSHINRQDIIFWVGYSASPDLSKLYKNCPRKARLVADCVKKYKEERPLFP 600
QY 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSRPLPVF 648
DB 601 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTTSRPLPVF 648

RESULT 4
ID KRAF_XENLA STANDARD; PRT; 638 AA.
AC P09560; Q91390;

```

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DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RAF proto-oncogene serine/threonine-protein kinase (EC 2.7.1.1.-).
DE C-RAF.
GN Xenopus laevis (African clawed frog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocyte;
RX MEDLINE=90057471; PubMed=3194203;
RA le Guellec R., le Guellec K., Paris J., Philippe M.;
RT "Nucleotide sequence of Xenopus C-raf coding region.";
RN Nucleic Acids Res. 16:10357-10357(1988).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92096753; PubMed=1721855;
RA le Guellec R., Couturier A., le Guellec K., Paris J., le Fur N.,
RA Philippe M.;
RT "Xenopus c-raf proto-oncogene: cloning and expression during
RT oogenesis and early development.";
RN Biol. Cell 72:39-45(1991).
CC -|- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS FROM
CC THE CELL MEMBRANE TO THE NUCLEUS. PART OF THE RAS-DEPENDENT
CC SIGNALING PATHWAY FROM RECEPTORS TO THE NUCLEUS.
CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MIL/RAF SUBFAMILY.
CC -|- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC BINDING DOMAIN.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC
CC EMBL; X12948; CAA31407.1; -.
CC PIR; S01930; TVLRF.
CC HSP; P04049; IFR.
CC InterPro; IPR002219; DAG_PE-bind.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR003116; RBD.
CC InterPro; IPR004040; STY_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF00130; DAG_PE-bind; 1.
CC Pfam; PF02196; RBD; 1.
CC PRINTS; PR00008; DAGPEDOMAIN.
CC ProDom; PD000001; Euk_pkinase; 1.
CC SMART; SM00109; C1; 1.
CC SMART; SM00455; RBD; 1.
CC SMART; SM00221; STYK; 1.
CC PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
CC PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;
KW ATP-binding; Phorbol-ester binding.
FT DOMAIN 138 183 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 340 600 PROTEIN KINASE.
FT NP_BIND 346 354 ATP (BY SIMILARITY).
FT BINDING 366 366 ATP (BY SIMILARITY).
FT ACT_SITE 459 459 BY SIMILARITY.
FT CONFLICT 309 309 K -> R (IN REF. 2).
SQ SEQUENCE 638 AA; 71959 MW; 1FF352BFFBF528DF CRC64;

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Query Match 84.5%; Score 2885; DB 1; Length 638;
Best Local Similarity 85.3%; Pred. No. 1.6e-187;
Matches 553; Conservative 35; Mismatches 50; Indels 10; Gaps 4;

QY 1 MEHIOGAKTISNGFGPRDAVDGSSCISPTIVQFGYORRASDDGLTDPKTSNTIRV 60
DB 1 MEHIOGAKTISNGFGPRDAVDGSSCISPTIVQFGYORRASDDGLTDPKTSNTIRV 60
QY 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFRLHHEHKKARLDWNTDAAS 120
DB 61 FLPNKQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFRLHHEHKKARLDWNTDAAS 120
QY 121 LIGBELVDLHDVPLTHNPAFTFLKLAFCDCIQKFLNGFRCTCG 180
DB 121 LIGBELVDLHDVPLTHNPAFTFLKLAFCDCIQKFLNGFRCTCG 180
QY 181 PTMCVDSNIRQLLFPNSTIGDSVPALPSLTHRRMRESVSRMPVSSQHRYPHAF 240
DB 181 PTMCVDSNIRQLLFPNSTIGDSVPALPSLTHRRMRESVSRMPVSSQHRYPHAF 240
QY 238 PTMCVDSNIRQLLFPNNEGSHLPSLTMRIGESV-RIPVSSQORISTPHPSF 238
DB 238 PTMCVDSNIRQLLFPNNEGSHLPSLTMRIGESV-RIPVSSQORISTPHPSF 238
QY 241 NTSPSSSEGLSQRSTSTPNVHMVSTLPVDSRMIEDAIRSHSESASPSSPNNL 300
DB 241 NTSPSSSEGLSQRSTSTPNVHMVSTLPVDSRMIEDAIRSHSESASPSSPNNL 300
QY 301 SPTGHSQKTPVPAQRERAPVSGTQENKIRPCQRDSSYYWEIEASEVMSLGRIGSGSF 360
DB 301 SPTGHSQKTPVPAQRERAPVSGTQENKIRPCQRDSSYYWEIEASEVMSLGRIGSGSF 360
QY 351 SPTGHSQKTPVPAQRERAPVSGTQENKIRPCQRDSSYYWEIEASEVMSLGRIGSGSF 351
DB 351 SPTGHSQKTPVPAQRERAPVSGTQENKIRPCQRDSSYYWEIEASEVMSLGRIGSGSF 351
QY 420 GTVYKKGWGDVAVKILKAVDPTPEQAFNEVAVLKRTHVNILLFMGVTMDNLAIV 420
DB 420 GTVYKKGWGDVAVKILKAVDPTPEQAFNEVAVLKRTHVNILLFMGVTMDNLAIV 420
QY 480 TOWCEGSSLYKHLHVQETKFMQFOLIDARQAGMDYLAHAKNIHHRDKSNIFLHEGL 480
DB 480 TOWCEGSSLYKHLHVQETKFMQFOLIDARQAGMDYLAHAKNIHHRDKSNIFLHEGL 480
QY 540 TVKIGDFGLATVSRWSGSOQVEQPTGSLVMAPEVIRMQDNNPFQSDVYSGIVLYE 540
DB 540 TVKIGDFGLATVSRWSGSOQVEQPTGSLVMAPEVIRMQDNNPFQSDVYSGIVLYE 540
QY 531 TVKIGDFGLATVSRWSGSOQVEQPTGSLVMAPEVIRMQDNNPFQSDVYSGIVLYE 531
DB 531 TVKIGDFGLATVSRWSGSOQVEQPTGSLVMAPEVIRMQDNNPFQSDVYSGIVLYE 531
QY 600 LMTGELPYSHINRDQIIFVGRGVYASPDLSKLYKNCPKAMKRLVADCVKVKERPLFP 600
DB 600 LMTGELPYSHINRDQIIFVGRGVYASPDLSKLYKNCPKAMKRLVADCVKVKERPLFP 600
QY 591 LMTGELPYSHINRDQIIFVGRGVYASPDLSKLYKNCPKAMKRLVADCVKVKERPLFP 591
DB 591 LMTGELPYSHINRDQIIFVGRGVYASPDLSKLYKNCPKAMKRLVADCVKVKERPLFP 591
QY 648 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPKLPVF 648
DB 648 QILSSIELLOHSLPKINRSASEPSLHRAAHTEDINACTLTSPKLPVF 648

RESULT 5

KRAA_PIG STANDARD: PRT; 606 AA.
ID KRAA_PIG
AC O19004;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE A-Raf proto-oncogene serine/threonine-protein kinase (EC 2.7.1.-)
DE (A-Raf-1).
GN ARAF1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Landrace; TISSUE=Liver;
RX MEDLINE=97343844; PubMed=9166601;
RA Yasue H., Adams L., Ozawa A., Hanazono M., Li N., Lin Z.H.,
RA Kusumoto H.;
RT "Assignment of ARAF1 to porcine chromosome Xp11.2-pl3 by fluorescence
RT in situ hybridization";
RL Mamm. Genome 8:457-458 (1997).
CC -!- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS

FROM THE CELL MEMBRANE TO THE NUCLEUS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
MIL/RAF SUBFAMILY.
-!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
BINDING DOMAIN.

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or send an email to license@isb-sib.ch).

EMBL: D88385; BAA232379.1; -
HSSP: P04049; 1FAR.
DR InterPro: IPR002219; DAG_PE-bind.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003116; RBD.
DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00130; DAG_PE-bind; 1.
DR Pfam: PF02196; RBD; 1.
DR PRINTS: PR00008; DAGPEDOMAIN.
DR PRODOM: PD000001; Euk_pkinase; 1.
DR SMART: SM00109; C1; 1.
DR SMART: SM00455; RBD; 1.
DR SMART: SM00221; STYK; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_SF; 1.
KW Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;
ATP-binding; Phorbol-ester binding.
FT DOMAIN 99 144 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 310 570 PROTEIN KINASE.
FT NP_BIND 316 324 ATP (BY SIMILARITY).
FT BINDING 336 336 ATP (BY SIMILARITY).
FT ACT_SITE 429 429 BY SIMILARITY.
SQ SEQUENCE 606 AA; 67538 MW; 1A7EB9A5D9DE152 CRC64;

Query Match 55.5%; Score 1893.5; DB 1; Length 606;
Best Local Similarity 60.9%; Pred. No. 1.4e-120;
Matches 375; Conservative 80; Mismatches 120; Indels 41; Gaps 9;

QY 50 DPSTSTNTIRVLPNKTQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFRLHHEHKK 109
DB 13 EPSRAVGTVKVYLPNKTQRTVVNVRNGMSLHDCMLKALKVRGLQPECCAVFRLHHEHKK 69
QY 110 ARLDWNTDAASLIGELQVDFLDHVPLTHNPAFTFLKLAFCDCIQKFLNGFRCTCG 169
DB 70 TVTAWDTAIPDLGEELIVELEDVPLTHNPAFTFLKLAFCDCIQKFLNGFRCTCG 129
QY 170 YKFEHCSTKVPKVCMDWS-NIRQLLFPNSTIGDSVPALPSLTHRRMRESVSRMPVSS 228
DB 130 YKFEHCSTKVPKVCMDWS-NIRQLLFPNSTIGDSVPALPSLTHRRMRESVSRMPVSS 187
QY 229 QHRYSTPHAFNTSTSPSSSEGLSQRSTSTPNVHMVSTLPVDSRMIEDAIRSHSES 288
DB 188 CTQHRDPEHPFP-----PAPANAPLQIRSTSTPNVHMVSTLPVDSRMIEDAIRSHSES 243
QY 289 -----SPSALSS-----SPNNLSPTGWSQKPTPVPAQRERAPVSGTQENK 330
DB 244 AGNRGGDGPAGPCSPSPASVSSGRKSPHKSPPS-----EQERKSLA---DDKKV 291
QY 331 RPRQRDSSYYWEIEASEVMSLSTRIGSGFGTGYKKGWGDVAVKILKVAQPTAEQAF 390
DB 292 KNLGRDSSYYWEIEASEVMSLSTRIGSGFGTGYKKGWGDVAVKILKVAQPTAEQAF 351
QY 391 RNEAVLKRTHRVNILLFMGVTMDNLAIVTQWCEGSSLYKHLHVQETKFMQFOLIDAR 450
DB 391 RNEAVLKRTHRVNILLFMGVTMDNLAIVTQWCEGSSLYKHLHVQETKFMQFOLIDAR 450

Db 352 KNEOVLRKTRHYNILLFMGEMTRPGFAITQWCEGSSLYHLHVADTRFDMVQLIDVAR 411

Qy 451 QTAQGDYHLAKNIIHRDMKSNFIHLHGLTVKIGDFGLATVKSRWGSQQVQPTGSGVL 510

Db 412 QTAQGDYHLAKNIIHRDLKSNFIHLHGLTVKIGDFGLATVKTRWSGAQPLEQPSGSGVL 471

Qy 511 WMAPEVIRMDNPNFSQSDVSYGIVLYELMTGELPYSHINRDQIIFMVGRYASDPL 570

Db 472 WMAEVRMDNPNFSQSDVSYGIVLYELMTGELPYSHINRDQIIFMVGRYASDPL 531

Qy 571 SKLYKNCPRKAMRLVADCVKVKKEERPLFPQILSSIELLQHSPLKINRSASEPSLHRAH 630

Db 532 SKLSSNCPKAMRLVADCVKVKKEERPLFPQILSSIELLQHSPLKINRSASEPSLHRAH 630

Qy 631 TEDINACTLTSPLRP 646

Db 591 ADELPACLLSAARLVP 606

RESULT 6

KRAA_RAT

ID KRAA_RAT STANDARD; PRT; 604 AA.

AC P14056;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE A-Raf proto-oncogene serine/threonine-protein kinase (EC 2.7.1.-).

GN ARAF1 OR A-RAF.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N. A.

RC STRAIN=Fischer; Tissus=Liver;

RX MEDLINE=88217324; PubMed=3449797;

RA Ishikawa F., Takaku F., Nagao M., Sugimura T.;

RT "The complete primary structure of the rat A-raf cDNA coding region: conservation of the putative regulatory regions present in rat C-raf.";

RT C-raf.";

RL Oncogene Res. 1:243-253(1987).

CC -1- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS FROM THE CELL MEMBRANE TO THE NUCLEUS.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC MTL/RAF SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG BINDING DOMAIN.

CC -----

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CC -----

DR EMBL: X06942; CAA30023.1; ..

DR PIR: S00726; S00726.

DR HSP: P04049; 1FAR.

DR InterPro: IPR002219; DAG_PE-bind.

DR InterPro: IPR000719; Euk_pkinase.

DR InterPro: IPR003116; RBD.

DR InterPro: IPR004040; STY_pkinase.

DR InterPro: IPR002290; Ser_thr_pkinase.

DR Pfam: PF00069; pkinase; 1.

DR Pfam: PF00130; DAG_PE-bind; 1.

DR Pfam: PF02196; RBD; 1.

DR PRINTS: PR000008; DAGPEDOMAIN.

DR ProDom: PD000001; Euk_pkinase; 1.

DR SMART: SM00109; Cl; 1.

DR SMART: SM00455; RBD; 1.

DR SMART: SM00221; STYK; 1.

DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.

DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;

KW ATP-binding; Phorbol-ester binding.

FT DOMAIN 99 144 PHORBOL-ESTER AND DAG BINDING.

FT DOMAIN 308 568 PROTEIN KINASE.

FT NP_BIND 314 322 ATP (BY SIMILARITY).

FT BINDING 334 334 ATP (BY SIMILARITY).

FT ACT_SITE 427 427 BY SIMILARITY.

SQ SEQUENCE 604 AA; 67551 MW; FF24FB2170B0B115 CRC64;

Query Match 55.4%; Score 1891.5; DB 1; Length 604;

Best Local Similarity 61.7%; Pred. No. 1.9e-120;

Matches 377; Conservative 76; Mismatches 125; Indels 33; Gaps 10;

Qy 50 DPKSTNTIRVFLPNKORTVNVNRNGMSLHDLCKALKVRGLQPECCAVFLLHEHGKK 109

Db 13 EFSRANGTVKVLPNKORTVTVRDGMSVDSLDALKVRGLNQDCCVTVRLI---KGRK 69

Qy 110 ARLDWNTDAASLIGEELQVDFLDHVPLTTHNFARKTEFLKAFCDICQKFLNGFRCTCG 169

Db 70 TVTAWDTAIAPLDGEELIVELEVDPLTMHNFVKTFEFLAFCDLFLFHGFCOTCG 129

Qy 170 YKFEHSTKVTPTMCVDS-NIQLLLPNTSGDGVPLPALPSLTMRMRMSVSRMPVSS 228

Db 130 YKFEHSTKVTPTMCVDS-NIQLLLPNTSGDGVPLPALPSLTMRMRMSVSRMPVSS 178

Qy 229 QHRYSTHAF-----FNTSSPSEGSLSQRSTSTPNVHMVSTTLTPVDSRMIEDAIRS 283

Db 179 LLTQGSFPFQQRDQEHFSPAPNPPLQKIRSTSTPNVHMVSTTAPDSSLMQFQAQS 238

Qy 284 HSESA-----SPSALSSSPNLSPTGWSQKTPVPA-QERAPVSGTQEKKIRPRGQ 335

Db 239 FSTDAAGRGDGPARG-SPSPASVS-SGRKSPHSLPAEQERKSLA--DEKKVKNLGY 294

Qy 336 RDSYYEIEIASFVNLSTRIGSGSGFGTVYKQHGVDVAVKILKVVDTPPQQAFAFRNEVA 395

Db 295 RDSYYEIEIEIASFVNLSTRIGSGSGFGTVYKQHGVDVAVKILKVVDTPPQQAFAFRNEQ 354

Qy 396 VLRTRVNIILFMGYNTKDLAIVTQWCESSLYKHLHVQETKQFQDLIDARQTAQG 455

Db 355 VLRTRVNIILFMGYNTKDLAIVTQWCESSLYKHLHVQETKQFQDLIDARQTAQG 414

Qy 456 MDYLHAKNIIHRDMKSNFIHLHGLTVKIGDFGLATVKSRWGSQQVQPTGSGVLMNAPE 515

Db 415 MDYLHAKNIIHRDLKSNFIHLHGLTVKIGDFGLATVKSRWGAQPLEQPSGSGVLMNAE 474

Qy 516 VIRMQDNPFSQSDVSYGIVLYELMTGELPYSHINRDQIIFMVGRYASDPLSKLYK 575

Db 475 VIRMQDNPFSQSDVSYGIVLYELMTGELPYSHINRDQIIFMVGRYASDPLSKLYK 534

Qy 576 NCPKAMRLVADCVKVKKEERPLFPQILSSIELLQHSPLKINRSASEPSLHRAHEDIN 635

Db 535 NCPKAMRLVADCVKVKKEERPLFPQILSSIELLQHSPLKINRSASEPSLHRAHEDIN 635

Qy 636 ACTLTSPLRP 646

Db 594 ACLLSARLVP 604

RESULT 7

ID KRAA_MOUSE STANDARD; PRT; 604 AA.

AC P04627; Q99J44; Q9CTT5; Q9D6R6; Q9DBU7;

DT 13-AUG-1987 (Rel. 05, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DE A-Raf proto-oncogene serine/threonine-protein kinase (EC 2.7.1.-).

GN ARAF1 OR ARAF OR A-RAF.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-283 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue, and Urinary bladder;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saio T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Hoffrelli D., Bojuno N., Carninci P., de Bona M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE OF 168-604 FROM N.A.
RX MEDLINE=87064566; PubMed=3491291;
RA Huleihel M., Goldsborough M., Cleveland J., Gunnell M., Bonner T.,
RA Rapp U.R.;
RT "Characterization of murine A-raf, a new oncogene related to the
RT v-raf oncogene.";
RL Mol. Cell. Biol. 6:2655-2662(1986).
CC -|- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS
CC FROM THE CELL MEMBRANE TO THE NUCLEUS.
CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MIL/RAF SUBFAMILY.
CC -|- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC BINDING DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: BC004757; AA04757.1; -;
DR EMBL: AK004741; BAB23522.1; -;
DR EMBL: AK010060; BAB26674.1; -;
DR EMBL: AK020547; BAB32131.1; -;
DR EMBL: D00024; BAA00018.1; -;
DR EMBL: M13071; AAA37258.1; -;
DR PIR: A25382; TVMSRF.
DR HSP: P08631; 1AD5.
DR MGD: MGI:88065; Araf.
DR InterPro: IPR002219; DAG_pe-bind.
DR InterPro: IPR00719; Euk_pkinase.
DR InterPro: IPR003116; RBD.
DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00130; DAG_pe-bind; 1.
DR Pfam: PF02196; RBD; 1.
DR PRINTS: PR00008; DAGPEDOMAIN.
DR SMART: SM00109; Cl; 1.

DR SMART: SM00455; RBD; 1.
DR SMART: SM00221; STYK; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;
KW ATP-binding; Phorbol-ester binding.
FT DOMAIN 99 144 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 308 568 PROTEIN KINASE.
FT NP_BIND 314 322 ATP (BY SIMILARITY).
FT BINDING 334 334 ATP (BY SIMILARITY).
FT ACT_SITE 427 427 E -> K (IN REF. 3).
FT CONFLICT 169 169 S -> R (IN REF. 2; BAB23522/BAB26674).
FT CONFLICT 186 186 R -> L (IN REF. 3).
FT CONFLICT 326 326 R -> L (IN REF. 3).
SQ SEQUENCE 604 AA; 67581 MW; 05F8262F99DD087 CRC64;
Query Match 55.4%; Score 1890.5; DB 1; Length 604;
Best Local Similarity 61.5%; Pred. No. 2.3e-120;
Matches 376; Conservative 77; Mismatches 125; Indels 33; Gaps 10;
QY 50 DPSTKSTNTHVLPNKORTVNVYRNGMSLHDLCKALKVYRGLQPECCAVFLLHEHKGK 109
DB 13 EPSRAVGTWAKVILPDKQRTVTVVREGMSVYDLSLCKALKVYRGLNQDCCVIRLI---KGRK 69
QY 110 ARLDWNTDAASLGEELQVDFLDHVPITTHNFARKTEFLKAFCDICQKFLGNGFCQTGC 169
DB 70 TVTAWDTAIPDLGEELEIVLEDVPLTMHNFVKRTFFSLAFCDCLKFLHFGFCQTGC 129
QY 170 YKFEHCSTKVPKTCVDMWS-NIRQLLFPNSTGDSGVLPALPSLTVRRNRESVSRMPVS 228
DB 130 YKFEHCSSKVPKTCVDMSTNRQFVHSIQDLSGGS-----RQEAAPSNLVNE 178
QY 229 QHRYSTPHAF-----FTSSPSEGLSQRQSTSTPNVHVSTLTPVDNRMIADARS 283
DB 179 LLTPQGPSPTQQRQDEHFSFPANPPQIRKSTSTPNVHVSTLTPMDSSLMQPTAOS 238
QY 284 HSESA-----SPSALSSPNNLSPGTSQKTPVPA-QRERAPVSGTQENKIRPRGQ 335
DB 239 FSTDAAGRGDGPARG-SPSPASVS-SGRKSPHSKLPSEQRERKSLA--DEKKVKNLGY 294
QY 336 RDSSTYWEIEASEVMLSTRIGSGFTGVYKGVHGDVAVKILKVDPTEPQFOAFNEVA 395
DB 295 RDSGYWEVPPSEVQLLKRICTGSGFTGVFRGHWGDVAVKLVKVAQPTAEQAQAFKNEQ 354
QY 396 VLKTRHVNILLFPGVYTKDNLAIYQWCEGSSLYKHLVQETKFMFOLIDFARQAG 455
DB 355 VLKTRHVNILLFPGVYTKDNLAIYQWCEGSSLYKHLVQETKFMFOLIDFARQAG 414
QY 456 MDYLHAKNIITHRDMKNINFLHGLVAVKIGDFGLATVKSWSGSGQVEQPTGSLVMAPE 515
DB 415 MDYLHAKNIITHRDLKNNIFLHGLVAVKIGDFGLATVKSWSGSGQVEQPTGSLVMAPE 474
QY 516 VIRMQDNPFSQSDVYSGIVLYELMTGELPYSVHNNRQIIFVGVGRGVSADPLSKLYK 575
DB 475 VIRMQDNPYSFQSDVYAYGVWLYELMTGSLPSYSHIGSRDQIIFVGVGRYSPDLKSF 534
QY 576 NCPKAMKRLVADCVKVKKEERPLFPQILSSIELQLHSLPKINRSASEPSLHRAAHTEDIN 635
DB 535 NCPKAMKRLVADCVKVKKEERPLFPQILSSIELQLHSLPKINRSASEPSLHRAAHTEDIN 593
QY 636 ACTITTSPLRP 646
DB 594 ACLLSAARLVP 604
RESULT 8
KRAA_HUMAN
ID KRAA_HUMAN STANDARD; PRT; 606 AA.
AC P10398; P07557;
DT 01-APR-1988 (Rel. 07, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE (A-raf proto-oncogene serine/threonine-protein kinase (EC 2.7.1.1-))
 GN ARAF1 OR PKS OR PKS2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RX MEDLINE=87146380; PubMed=3029685;
 RA Beck T.W., Huleihel M., Gunnell M., Bonner T.L., Rapp U.R.;
 RT "The complete coding sequence of the human A-raf-1 oncogene and
 RL Nucleic Acids Res. 15:595-609(1987)."
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=94292185; PubMed=8020955;
 RA Lee J.-E., Beck T.W., Brennscheidt U., DeGennaro L.J., Rapp U.R.;
 RT "The complete sequence and promoter activity of the human A-raf-1
 RL gene (ARAF1).";
 RN Genomics 20:43-55(1994).
 RP SEQUENCE OF 292-589 FROM N.A.
 RX MEDLINE=86313571; PubMed=3529082;
 RA "Pks, a raf-related sequence in humans.";
 RT Proc. Natl. Acad. Sci. U.S.A. 83:6312-6316(1986).
 CC -!- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS
 CC FROM THE CELL MEMBRANE TO THE NUCLEUS.
 CC -!- TISSUE SPECIFICITY: PREDOMINANTLY IN UROGENITAL TISSUES (BY
 CC SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC BINDING DOMAIN.
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 CC
 DR EMBL; X04790; CAA28476.1; -;
 DR EMBL; L24038; AAA65219.1; -;
 DR EMBL; U01337; AAB03517.1; -;
 DR EMBL; M13829; AAB08754.1; -;
 DR PIR; A26439; TVHDAF.
 DR PIR; A23541; TVHDPK.
 DR HSP; P04049; IFAR.
 DR Genew; HGNC:646; ARAF1.
 DR MIM; 311010; -;
 DR InterPro; IPR002219; DAG_PE-bind.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003116; RBD.
 DR InterPro; IPR004040; STY_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00130; DAG_PE-bind; 1.
 DR Pfam; PF02196; RBD; 1.
 DR PRINTS; PR00008; DAGPEDOMAIN.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00109; C1; 1.
 DR SMART; SM00455; RBD; 1.
 DR SMART; SM00221; STYK; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM.1; 1.
 DR PROSITE; PS00081; DAG_PE_BIND_DOM.2; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;
 KW ATP-binding; Phorbol-ester binding.
 FT DOMAIN 99 144 PHORBOL-ESTER AND DAG BINDING.
 FT DOMAIN 310 570 PROTEIN KINASE.
 FT NP_BIND 316 324 ATP (BY SIMILARITY).
 FT BINDING 326 336 ATP (BY SIMILARITY).
 FT ACT_SITE 429 439 BY SIMILARITY.
 FT CONFLICT 368 378 L -> P (IN REF. 3).
 FT CONFLICT 378 378 F -> V (IN REF. 3).
 FT CONFLICT 469 469 S -> P (IN REF. 3).
 FT CONFLICT 478 478 I -> T (IN REF. 3).
 SQ SEQUENCE 606 AA; 67585 MW; D23E5711304AA68 CRC64;
 Query Match 55.4%; Score 1889.5; DB 1; Length 606;
 Best Local Similarity 61.9%; Pred. No. 2.6e-120;
 Matches 376; Conservative 76; Mismatches 132; Indels 23; Gaps 9;
 QY 50 DPSKTSNTIRVFLPNKQRTVVNRGMSLHDCMLKALKVGRLOPECCAVFLLHEHCKK 109
 DB 13 EFSRAVGTVKVVLPNKRQRTVVNRGMSVYSLDKALKVGRGUNGQCCVVYRLI---RGRK 69
 QY 110 ARLDWNTDAASLIGELQVDFLDHVPFLTHNFARKFLKAFCDICQKFLNGFCQTCG 169
 DB 70 TVTAWDTAIAPLDGEELIVEVLEVDVPLTMHNFVKTFFSLAFCDCLFLFHGFCQTCG 129
 QY 170 YKFEHCSTKVTMCVDNSNIRQLLPNSTI-GDSGVPALESLTMRMRSSVSRMPVSS 228
 DB 130 YKPHQCSKVTVCVDMSTNRQVFVSHYQDLSGSGSRQHEAPS--NRPLNELLTPQGSP 187
 QY 229 QHRYSTPHAFNTSSPSSEGLSORSTSTPNVHMVSTTLPVDSRME-----DA 280
 DB 188 RQHCDEHPFP-----PAPANAPLQIRSTSTPNVHMVSTTAPMDSNLIQLTGQSFSDA 243
 QY 281 IRSHSESASPSSALSSPNLSTGWSQPKTPVPA-QRERAPVSGTQEKNKIRPRGQDSS 339
 DB 244 AGSRGSGDGTGRGSPSPASVS-SGRKSPHSKSPAQRERKSLA--DDKKVKNLGYRDSG 300
 QY 340 YWEIEASEVMSLSTRIGSGFVYKGVHGDVAVKILKVVDPTPEQQAQFNEVAVLRK 399
 DB 301 YWEVPEVPSVQLLRIGTSGFVGRHGDVAVKLVKVSQPTAEQAQAFKNEQVLRK 360
 QY 400 TRHVNILLFMGYMTKDLAIVTQWCEGSLYKHLHVQETKFFOMFOLIDARTAGMDYL 459
 DB 361 TRHVNILLFMGYMTKPGFAITQWCEGSLYHLLHVAVDTRFDMVOLIDVARCTAGMDYL 420
 QY 460 HAKNIITHRDMKNNIFLHEGLVFKIGDGLATVTKRWSGSSQVQPTQSVLMAPEVIRM 519
 DB 421 HAKNIITHRDLKSNIFLHEGLVFKIGDGLATVTKRWSGAQPLEQPSGSLVMAAEVIRM 480
 QY 520 QDNPPFSQSDVYSYGVLYELMTGELPYSHNNRDOIFEMVGRGYASPDLSKLYKNCPK 579
 DB 481 QDPNPYSQSDVYAYGVLYELMTGELPSLPSYSHGCRDQIFEMVGRGYLSPDLSKISSNCPK 540
 QY 580 AMKRLVADCVKVKKEERPLFPQILSSIELLOHSLPKINRSASEPSLHRAATEDINACTL 639
 DB 541 AMRRLSDCLKFQREERPLFPQILATIELLQSLPKIERSASEPSLHR-TQADELPACIL 599
 QY 640 TTSPLRP 646
 DB 600 SAARLYP 606
 RESULT 9
 KMLAVIMH STANDARD; PRT; 380 AA.
 ID KMLAVIMH
 AC P00531;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Serine/threonine-protein kinase transforming protein ml
 DE (EC 2.7.1.37).
 GN V-MIL OR V-MHT.

OS Avian retrovirus MH2.
 OC Viruses; Retroviridae; Alpharetrovirus.
 OC NCBI_TaxID=11870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84191511; PubMed=6325930;
 RA Sutcliffe P., Bonner T.I., Rapp U.R., Jansen H.W., Patschinsky T.,
 RA Bister K.;
 RT "Nucleotide sequence of avian retroviral oncogene v-mil: homologue of
 RT murine retroviral oncogene v-raf";
 RL Nature 309:85-88(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84121298; PubMed=6320371;
 RA Kan N.C., Flordellis C.S., Mark G.E., Duesberg P.H., Papas T.S.;
 RA "A common oncogene sequence transduced by avian carcinoma virus MH2
 RT and by murine sarcoma virus 3611";
 RL Science 223:813-816(1984).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
 CC -1- DISEASE: BY ITSELF THE V-MIL ONCOGENE HAS ONLY WEAK TRANSFORMING
 CC CAPACITY BUT IT ABOLISHES THE GROWTH FACTOR REQUIREMENTS OF AVIAN
 CC MACROPHAGES TRANSFORMED BY OTHER ONCOGENES.
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-MT OR GAG-MIL
 CC POLYPEPTIDE.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MIL/RAF SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: X00534; CAA25211.1; ALT_INIT.
 DR PIR: A00639; TVFVW.
 DR HSP: P08631; IADS.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR004040; STY_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00221; STYK; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PolyProtein: Serine/threonine-protein kinase; Transferase; Oncogene;
 KW ATP-binding.
 FT DOMAIN 82 341 PROTEIN KINASE.
 FT NP_BIND 88 96 ATP (BY SIMILARITY).
 FT BINDING 108 108 ATP (BY SIMILARITY).
 FT ACT_SITE 201 201 BY SIMILARITY.
 FT CONFLICT 211 211 G -> E (IN REF. 2).
 SQ SEQUENCE 380 AA; 42853 MW; 6498695FB7EBE5D CRC64;
 Query Match 55.3%; Score 1888.5; DB 1; Length 380;
 Best Local Similarity 94.7%; Pred. No. 1.7e-120;
 Matches 360; Conservative 12; Mismatches 7; Indels 1; Gaps 1;
 QY 269 TLPVDSRMIEDAIRSHSEASPSALSSSPNNISPTGWSQPKTPVPAQERAPVSGTQKN 328
 Db 2 THPVDSEIIEAIRNHSSEASPSASGSPNNISPTGWSQPKTPVPAQERAPVSGTQKN 61
 QY 329 KIRPGQDSYYWEIEASEVMSLSTRIGSGFTYKKGWGDVAVKILKVVDPPPEQFQ 388
 Db 62 KIRPGQDSYYWEIEASEVMSLSTRIGSGFTYKKGWGDVAVKILKVVDPPPEQFQ 121
 QY 389 AFRNEVAVLRKTHVNLIFMGMKNDLAIYVQNCESGLYKHLHVQETKFMQLIDI 448
 Db 122 AFRNEVAVLRKTHVNLIFMGMKNDLAIYVQNCESGLYKHLHVQETKFMQLIDI 181
 QY 449 ARQTAQGMDFLHAKNIHHRDKMKNIFLHGGLTVKIGDFLATVKSRSQSQVEQPTGS 508

Db 192 ARQTAQGMDFLHAKNIHHRDKMKNIFLHGGLTVKIGDFLATVKSRSQSQVEQPTGS 241
 QY 509 VLMAPEVIRMDNNPFSQSDVSYGIVLYELMTGELPYSHINNRDQIIFWVGKGYASP 568
 Db 242 ILMAPEVIRMDNSNPFQSDVSYGIVLYELMTGELPYSHINNRDQIIFWVGKGYASP 301
 QY 569 DLSKLYKNCPRAMKRLVADCVKVKKEERPLFPQILSSIELLOHSLPKINRSASEPFLHRA 628
 Db 302 DLSKLYKNCPRAMKRLVADCVKVKKEERPLFPQILSSIELLOHSLPKINRSASEPFLHRA 361
 QY 629 AHTEIDINACTLTTSPLPVE 648
 Db 362 SHTEIDINACTLT-TSTRLPVF 380
 RESULT 10
 KRAB_HUMAN
 ID KRAB_HUMAN STANDARD; PRT; 765 AA.
 AC P15056;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE B-raf proto-oncogene serine/threonine-protein kinase (EC 2.7.1.-)
 DE (p94) (v-Raf murine sarcoma viral oncogene homolog B1).
 GN BRAF OR BRAF1 OR RAFB1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Testis;
 RX MEDLINE=923735040; PubMed=1508179;
 RA Stephens R.M., Sthanandam G., Copeland T.D., Kaplan D.R., Rapp U.R.,
 RA Morrison D.K.;
 RT "95-kilodalton B-Raf serine/threonine kinase: identification of the
 RT protein and its major autophosphorylation site";
 RL Mol. Cell. Biol. 12:3733-3742(1992).
 RN [2]
 RP SEQUENCE OF 116-765 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=91133728; PubMed=2284096;
 RA Sthanandam G., Kolch W., Duh F.-M., Rapp U.R.;
 RT "Complete coding sequence of a human B-raf cDNA and detection of
 RT B-raf protein kinase with isozyme specific antibodies";
 RL Oncogene 5:1775-1780(1990).
 RN [3]
 RP SEQUENCE OF 438-765 FROM N.A.
 RX MEDLINE=88302178; PubMed=3043188;
 RA Ikawa S., Fukui M., Ueyama Y., Tamaoki N., Yamamoto T., Toyoshima K.;
 RT "B-raf, a new member of the raf family, is activated by DNA
 RT rearrangement";
 RL Mol. Cell. Biol. 8:2651-2654(1988).
 CC -1- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS
 CC FROM THE CELL MEMBRANE TO THE NUCLEUS.
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE POSTSYNAPTIC RESPONSES OF
 CC HIPPOCAMPAL NEURON.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: CEREBRUM AND TESTES.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MIL/RAF SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC BINDING DOMAIN.
 CC -----
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 CC -----

DR EMBL; M95712; AAA35609.1; -;
 DR EMBL; M21001; AAA96495.1; -;
 DR PIR; A31850; TVHUBF.
 DR PIR; S13798; S13798.
 DR HSSP; P04049; 1FAR.
 DR Genew; HGNC:1097; BRAF.
 DR MIM; 164757; -;
 DR InterPro; IPR002219; DAG_PE-bind.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003116; RBD.
 DR InterPro; IPR004040; STY_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00130; DAG_PE-bind; 1.
 DR Pfam; PF02196; RBD; 1.
 DR PRINTS; PRO0008; DAGPEDOMAIN.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00109; C1; 1.
 DR SMART; SM00455; RBD; 1.
 DR SMART; SM00221; STYK; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;
 KW ATP-binding; Phorbol-ester binding; Phosphorylation.
 FT DOMAIN 6 11
 FT DOMAIN 121 128
 FT DOMAIN 234 279
 FT DOMAIN 427 431
 FT DOMAIN 456 716
 FT NP_BIND 462 470
 FT BINDING 482 482
 FT ACT_SITE 575 575
 FT MOD_RES 372 372
 FT CONFLICT 765 765
 FT SEQUENCE 765 AA; 84490 MW; 93A9EE4D6C1C68E CRC64;
 Query Match 53.5%; Score 1825; DB 1; Length 765;
 Best Local Similarity 56.7%; Pred. No. 8.2e-116;
 Matches 379; Conservative 80; Mismatches 167; Indels 42; Gaps 13;
 QY 9 KRISNGFGFK-----DAVFGSSCSPTIVQFGYORRSDCKLTPDKSTNIWVF 61
 DB 100 ESLNGTDFSVSSASMDTVTSSSSLSVLSPSSLSVFNPTDVARSPKSPQKPIWVF 159
 QY 62 LPNKQRTVYVNRGMSLDLMLKALKVRGLQPECCAVFRLHHEHKKARLDWNTDAASL 121
 DB 160 LPNKQRTVVPARGVTVDLSKALMMRGLIPECCAVYRI---QDGEKKPIGWDTDISWL 216
 QY 122 IGEELQVDFLDHVLTHNFARKTFKLAFCDICQKFLNGPRCQTCGYKPKHEHCSTKVP 181
 DB 217 TGEELVEVLEYNPLTHNFARKTFKLAFCDICQKFLNGPRCQTCGYKPKHEHCSTKVP 276
 QY 182 TWCVDNRSRQLLFPNLTIGSDVP-----ALPSLTMRMRRESVSRMP---VSSQ 229
 DB 277 LMCVNDQLD--LLFVSKFEHHPHQEASLAETALTSGSPSPAPSDSGPQLITSPS 334
 QY 230 HRYSTPHAFNTSPSSSEGLSQRSSTPTNVHMTTLTPVDSRMIEDAIRS---HSE 286
 DB 335 PSKSIPFPFRPAEDHNRNQGRDRSSAPNVH-INTIEPVN---IDDLIRDOQGRGD 390
 QY 287 SASPSALSSPNLSPTGHSQ----PKTPVPAQRERAPVSGTQKNTKPRGCRDSSYYW 342
 DB 391 GGGTTLGSLATPPLSGSLTNVYKALQKSPG-ORERKSSSSSESDNRNMTLGRDSSDDW 449
 QY 343 ETEASEVSLTRIGSGSFGTVYKKGWHDVAVYKLVVDPTPEQFAFRNEAVLKRTRH 402
 DB 450 EIPDGGIITVQRLGSGSFGTVYKKGWHDVAVYKLVNVTAPTQQLQAFNEVGLKRTRH 509
 QY 403 VNILLPMGYMTKDNLAIVTQWCEGSSLYHLHVFQETKFMFOLDIARTAGMDYLHAK 462

Db 510 VNILLPMGYSTKPOLAIVTQWCEGSSLYHLHVFQETKFMFOLDIARTAGMDYLHAK 569
 QY 463 NIIHRDKSNFIHLEGLTVKIGDFGLATVYKSRWSGSGQVEQPTGSLVWMAPEVIRMQDN 522
 DB 570 SIIHRDLKSNFIHLEGLTVKIGDFGLATVYKSRWSGSHQFEQLSGSILWMAPEVIRMQDK 629
 QY 523 NPFSFQSDVYSYGVILYELMTGELPYSNRRDQIIFMVGRGYASPDLSKLYKNCPKAMK 582
 DB 630 NPYSFQSDVYAFGVILYELMTGOLPYSNRRDQIIFMVGRGYASPDLSKLYKNCPKAMK 689
 QY 583 RLVADCVKVKERRPLFPQILSSILLOHSLPKINRSASEPSLHRAA--HTEDIN--ACTL 639
 DB 690 RLMAECLKKRDERPLFPQILASIELLARSPLKIHRSASEPSLNRAGFTQDEFSLYAC-- 747
 QY 640 TTSPLRPV 647
 DB 748 -ASPKTPI 754
 RESULT 11
 RMIL_CHICK
 ID RMIL_CHICK STANDARD; PRT; 806 AA.
 AC Q04982;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE RMIL serine/threonine-protein kinase (BC 2.7.1.37).
 OS C-RMIL.
 GN Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RC TISSUE-Lymphocytes, and Fibroblast;
 RC MEDLINE=93312327; PubMed=8323553;
 RX Calogeraki I., Barnier J.V., Eychene A., Felder M.-P., Calothy G.,
 RA Marx M.;
 RA "Genomic organization and nucleotide sequence of the coding region of
 the chicken c-Rnil(B-raf-1) proto-oncogene";
 RT Biochem. Biophys. Res. Commun. 193:1324-1331(1993).
 RL
 CC -1- FUNCTION: MAY PLAY A ROLE IN TRANSDUCING SPECIFIC SIGNALS IN
 NEURAL CELLS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
 SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEURAL TISSUE.
 CC -1- PTM: PHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER-BINDING
 BINDING DOMAIN.
 CC
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 CC
 CC EMBL; X67052; CAA47436.1; -;
 CC PIR; JN0612; JN0612.
 CC HSSP; P04049; 1FAR.
 CC InterPro; IPR002219; DAG_PE-bind.
 CC InterPro; IPR000719; Euk_pkinase.
 CC InterPro; IPR003116; RBD.
 CC InterPro; IPR004040; STY_pkinase.
 CC InterPro; IPR002290; Ser_thr_pkinase.
 CC Pfam; PF00069; pkinase; 1.
 CC Pfam; PF00130; DAG_PE-bind; 1.

```

Db      736 CLKKKRDEPLFPQILASIELLARSPLKIHRSSEPSLNLRAGQTFEDSLYAC-----ASPK 792
Qy      645 LPV 647
Db      793 TPI 795

RESULT 12
RMIL_COTJA
ID  RMIL_COTJA  STANDARD;  PRT;  807 AA.
AC  AC  P34908;
DT  01-FEB-1994 (Rel. 28, Created)
DT  01-FEB-1994 (Rel. 28, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  RMIL serine/threonine-protein kinase (EC 2.7.1.37).
GN  C-RMIL.
OS  Coturnix coturnix japonica (Japanese quail).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC  Coturnix.
OX  NCBI_TaxID=93934;
RN  [1]
SEQUENCE FROM N.A.
RX  MEDLINE=92319540; PubMed=1620546;
RA  Eychene A., Barnier J.V., Dezelee P., Marx M., Laugier D.,
RA  Calogeraki I., Calothy G.;
RT  "Quail neuroretina c-Rmil(B-raf) proto-oncogene cDNAs encode two
RT  proteins of 93.5 and 95 kDa resulting from alternative splicing.";
RT  Oncogene 7:1315-1323(1992).
RL  -1- FUNCTION: MAY PLAY A ROLE IN TRANSDUCING SPECIFIC SIGNALS IN
CC  NEURAL CELLS.
CC  -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC  -1- SUBCELLULAR LOCATION: Nuclear.
CC  -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC  SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC  -1- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEURAL TISSUE.
CC  -1- PTM: PHOSPHORYLATED.
CC  -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC  MIL/RAF SUBFAMILY.
CC  -1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC  BINDING DOMAIN.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; M80846; AAA49493.1; -;
CC  EMBL; M80845; AAA49492.1; -;
CC  HSSP; P04049; 1FAR.
CC  InterPro; IPR002219; DAG_PE-bind.
CC  InterPro; IPR000719; Euk_pkinase.
CC  InterPro; IPR003116; RBD.
CC  InterPro; IPR004040; STY_pkinase.
CC  InterPro; IPR002290; Ser_thr_pkinase.
CC  Pfam; PF00069; pkinase; 1.
CC  Pfam; PF00130; DAG_pe-bind; 1.
CC  Pfam; PF02196; RBD; 1.
CC  PRINTS; PR00008; DAGPEDOMAIN.
CC  ProDom; PD0000001; Euk_pkinase; 1.
CC  SMART; SM00109; C1; 1.
CC  SMART; SM00455; RBD; 1.
CC  SMART; SM00221; STYKc; 1.
CC  PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
CC  PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
CC  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC  PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC  PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC  PROTO-oncogene: Transferrase; Serine/threonine-protein kinase.

```


Db 181 TGSVLWMAPEVIRMQDDNPFQSDVYSYGVIVLYELMAGELPYAHANNRDIIFWVGROY 240
Qy 566 ASDLSKLYNCPKAMKRLVADCVKVKKEERPLFPQILSSIELLQHSKPKINRSASEPSL 625
D 241 ASDLSKLYNCPKAMKRLVADCVKVKKEERPLFPQILSSIELLQHSKPKINRSASEPSL 300
Qy 626 HRAAHTEDINACTLTSPRLPVF 648
D 301 HRAAHTEDINACTLTSPRLPVF 323

RESULT 14

KRAF_DROME STANDARD; PRT; 781 AA.
AC P11346;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RAF homolog serine/threonine-protein kinase drap-1 (EC 2.7.1.1-)
DE (hole-hole protein).
GN PHL OR DRAF-1 OR D-RAF.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

FN SEQUENCE FROM N.A.
RP MEDLINE=8823647; PubMed=3135183;
RA Nishida Y., Hata M., Ayaki T., Ryo H., Yamagata M., Shimizu K.,
RA Nishizuka Y.;
RT "Proliferation of both somatic and germ cells is affected in the
RT drosophila mutants of raf proto-oncogene.";
RL EMBO J. 7:775-781(1988).
RN (2)
RP SEQUENCE OF 465-753 FROM N.A.
RX MEDLINE=87257926; PubMed=3037346;
RA Mark G.E., Macintyre R.J., Digan M.E., Ambrosio L., Perrimon N.;
RA "Drosophila melanogaster homologs of the raf oncogene.";
RL Mol. Cell. Biol. 7:2134-2140(1987).
RN (3)
RP CHARACTERIZATION.
RX MEDLINE=93140754; PubMed=8423783;
RA Sprenger F., Torsocclair M.M., Morrison D.K.;
RT "Biochemical analysis of torso and D-raf during Drosophila
RT embryogenesis: Implications for terminal signal transduction.";
RL Mol. Cell. Biol. 13:1163-1172(1993).
CC -1- FUNCTION: SERINE/THREONINE KINASE REQUIRED IN THE EARLY EMBRYO
CC FOR THE FORMATION OF TERMINAL STRUCTURE. ALSO REQUIRED DURING
CC THE PROLIFERATION OF IMAGINAL CELLS. MAY ACT DOWNSTREAM OF RAS1
CC IN THE SEV SIGNAL TRANSDUCTION PATHWAY.
CC -1- PTM: EXTENSIVELY PHOSPHORYLATED AT 1 TO 2 H AFTER EGG LAYING.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MIL/RAF SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC BINDING DOMAIN.

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CC -----
DR EMBL: X07181; CAA30166.1; ALT INIT.
DR EMBL: M16598; -: NOT_ANNOTATED_CDS.
DR PIR: S00393; TVFDF.
DR HSP: P04049; IRFA.
DR FlyBase: FBgn0003079; phl.
DR InterPro: IPR002219; DAG_pe-bind.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003116; RBD.

DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00130; DAG_pe-bind; 1.
DR Pfam: PF02196; RBD; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00109; Cl; 1.
DR SMART: SM00455; RBD; 1.
DR SMART: SM00221; STYK; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE: PS0081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Zinc;
KW Phorbol-ester binding; Phosphorylation.
FT DOMAIN 265 310 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 471 732 PROTEIN KINASE.
FT NP_BIND 477 485 ATP (BY SIMILARITY).
FT BINDING 497 497 ATP (BY SIMILARITY).
FT ACT_SITE 590 590 P -> A (IN REF. 2).
FT CONFLICT 495 495 KKT -> RKA (IN REF. 2).
FT CONFLICT 520 522 G -> R (IN REF. 2).
FT CONFLICT 571 571 RRHS -> PQAL (IN REF. 2).
FT CONFLICT 700 703 DEAD54762249EADC CRC64;
SQ SEQUENCE 781 AA; 88794 MW; 54762249EADC CRC64;
Query Match 39.8%; Score 1360; DB 1; Length 781;
Best Local Similarity 46.3%; Pred. No. 2.2e-84;
Matches 303; Conservative 86; Mismatches 194; Indels 72; Gaps 16;
QY 32 IVQFGYQRRASDDGKLD-----PSKTSNT-----IRVFLPNKORTVVVNRGMSL 78
DB 146 ILQOORQLARVHGTDLTSLGSPGSCGTLTROPKILLRAHLNPOORTSVEVIGVRL 205
QY 79 HDCLMALKVGLQPECCAVFLLHEHKKARLDWNTDAALGEEQLQVDFLDHVLPT 138
DB 206 CDALMALKLRQLTDFMCEVST---THSGRHI-IPWHTDIGTHERVEEIVRLDFPINT 261
QY 139 ---HNFARKTFLKLAFCDCIKQKFLNGFCQCYKFKHEHCSTKYPTMCVDW--SNIRQL 193
DB 262 HIKHQIIRKTFEFLVFCGCRLLFTGYCSQCNFRHQRCANRVMLCQPPMDSYQL 321
QY 194 LLEPNSTICDGVLPALPSLTMRMRSEVSRVPSQHRYSTPHATFTSS--PSEGS- 250
DB 322 LLAEND---DNGY-GFPG-----RGTAVRFNMSSRSRRSSSSSSSSSSSSSGN 371
QY 251 -----LSQRSTSTPNV---HMVSTLPVDSRMIEDA-----IRSHSESASPSA 292
DB 372 HRQGRPRISQDRSNSAPNVCINNIRSVTSEVQSRSLNQARPLPHPCDHSNSTQSP 431
QY 293 LSSPPNLSPTGWSQPKTPVPAQRAPVSGTQEKNIKIRPGQRDSSYYWEIEASEVMLS 352
DB 432 TSTLKH-----RPRASDESNNKLL--RDAKSSSENNILAEILIG 474
QY 353 TRIGSSFGTVYKKGWHDVAVKILKVDPTEQFAFRNEVAVLKRTHVILLFMGYM 412
DB 475 PRIGSGFGTVYRAHVGPPVVKTLNVKTPSPAQLQAFKNEVAMLKLRHCHNILLFMGCV 534
QY 413 TKDNLAIVTQWCEGSSLYKHLHVQETKQFOMFOLIDIARTAOGMDYLAHKNIIHRDKSN 472
DB 535 SKPSLAIVTQWCEGSSLYKHLHVSETKFKLNTLIDIGROVAGMDYLAHKNIIHRDKSN 594
QY 473 NIFLHGLAVKIGDFGLATVKRWGSGQVQPTGSLVNAPEVIRMQDNNPFQSDVY 532
DB 595 NIFLHEDLSVKIGDFGLATAKTAWSEKQANQPTGSLVNAPEVIRMQDNNPFQSDVY 654
QY 533 SYGIVLYELMTGELPYSHINNRDQIIFWVGROYASPDLSKLYNCPKAMKRLVADCVK 592
DB 655 AFGIVMYELAECLPYGHISNKKDQILFWVGRLPDMSQVRSADARRHKKRAEDCIK 714
QY 593 KEERPLFPQILSSIELLQHSKPKINRSASEPSLHRAAHTEDINACTLTSPRLPV 647

